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<input type="checkbox"/>	L6	L5 and @pd > 20051011	3
<input type="checkbox"/>	L5	L4 and (divergen\$ or opposit\$)	36
<input type="checkbox"/>	L4	L3 same enhancer	46
<input type="checkbox"/>	L3	L1 or L2	411
<input type="checkbox"/>	L2	bi-direction\$ near3 (promoter or regulator\$ region or regulat\$ element or regulat\$ sequence)	129
<input type="checkbox"/>	L1	bidirection\$ near3 (promoter or regulator\$ region or regulat\$ element or regulat\$ sequence)	321

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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: Celine Qian Examiner #: 78710 Date: 5/30/06  
Art Unit: 1636 Phone Number: 2-0777 Serial Number: 10/075105  
Location (Bldg/Room#): 3D21 (Mailbox #): 2670 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Bi-directional dual promoter complex -  
Inventors (please provide full names): Li, Zhijian et al.

Earliest Priority Date: 2/13/2001

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 1 (both commercial & interference database). Thank you.

6/6/06

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1-736 na  
LB

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Searcher: Beverly C 2528 Type of Search: NA Sequence (#)

Searcher Phone #: \_\_\_\_\_ AA Sequence (#)

Searcher Location: \_\_\_\_\_ Structure (#)

Date Searcher Picked Up: \_\_\_\_\_ Bibliographic

Date Completed: \_\_\_\_\_ Litigation

Searcher Prep & Review Time: \_\_\_\_\_ Fulltext

Online Time: \_\_\_\_\_ Other

Vendors and cost where applicable

\_\_\_\_\_ STN \_\_\_\_\_ Dialog

\_\_\_\_\_ Questel/Orbit \_\_\_\_\_ Lexis/Nexis

\_\_\_\_\_ Westlaw \_\_\_\_\_ WWW/Internet

\_\_\_\_\_ In-house sequence systems CGN

\_\_\_\_\_ Commercial \_\_\_\_\_ Oligomer \_\_\_\_\_ Score/Length

\_\_\_\_\_ Interference \_\_\_\_\_ SPDI \_\_\_\_\_ Encode/Transl

\_\_\_\_\_ Other (specify)

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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 04:40:23 / Search time 528 Seconds

(without alignment)  
9718,892 Million cell updates/sec

Title: US-10-075-105C-1

Sequence: 1 ggaaccagcggtcctctcc.....ggagaggaacagctgagacc 736

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapexc 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 04  
Maximum Match 1004  
Listing first 45 summaries

Database :

N\_Geneseq\_8:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003s:.\*  
7: Geneseq2004s:.\*  
8: Geneseq2005s:.\*  
9: Geneseq2006s:.\*  
10: Geneseq2007s:.\*  
11: Geneseq2008s:.\*  
12: Geneseq2009s:.\*  
13: Geneseq2010s:.\*  
14: Geneseq2011s:.\*  
15: Geneseq2012s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	734.4	99.8	736	ABSS3103	ABSS3103 Transgene
2	597.4	81.2	1360	ABSS3105	ABSS3105 Transgene
3	554	75.3	661	AAH81003	AAH81003 Enhanced
4	554	75.3	661	AAH81010	AAH81010 Enhanced
5	554	75.3	2127	AAH81015	AAH81015 Enhanced
6	554	75.3	2127	AAH81015	AAH81015 Enhanced
7	554	75.3	2127	AAH81015	AAH81015 Enhanced
8	554	75.3	2127	AAH81015	AAH81015 Enhanced
9	554	75.3	2127	AAH81015	AAH81015 Enhanced
10	554	75.3	2127	AAH81015	AAH81015 Enhanced
11	554	75.3	2127	AAH81015	AAH81015 Enhanced
12	554	75.3	2127	AAH81015	AAH81015 Enhanced
13	554	75.3	2127	AAH81015	AAH81015 Enhanced
14	554	75.3	2127	AAH81015	AAH81015 Enhanced
15	554	75.3	2127	AAH81015	AAH81015 Enhanced
16	554	75.3	2127	AAH81015	AAH81015 Enhanced
17	554	75.3	2127	AAH81015	AAH81015 Enhanced
18	554	75.3	2127	AAH81015	AAH81015 Enhanced

19	554	75.3	8012	2	AAH57305	AAH57305 Sugar bee
20	554	75.3	8012	3	AAH57305	AAH57305 Sugar bee
21	554	75.3	8012	4	AAH57305	AAH57305 Sugar bee
22	554	75.3	8012	5	AAH57305	AAH57305 Sugar bee
23	554	75.3	8012	6	AAH57305	AAH57305 Sugar bee
24	554	75.3	8012	7	AAH57305	AAH57305 Sugar bee
25	554	75.3	8012	8	AAH57305	AAH57305 Sugar bee
26	554	75.3	8012	9	AAH57305	AAH57305 Sugar bee
27	554	75.3	8012	10	AAH57305	AAH57305 Sugar bee
28	554	75.3	8012	11	AAH57305	AAH57305 Sugar bee
29	554	75.3	8012	12	AAH57305	AAH57305 Sugar bee
30	554	75.3	8012	13	AAH57305	AAH57305 Sugar bee
31	554	75.3	8012	14	AAH57305	AAH57305 Sugar bee
32	554	75.3	8012	15	AAH57305	AAH57305 Sugar bee
33	554	75.3	8012	16	AAH57305	AAH57305 Sugar bee
34	554	75.3	8012	17	AAH57305	AAH57305 Sugar bee
35	554	75.3	8012	18	AAH57305	AAH57305 Sugar bee
36	554	75.3	8012	19	AAH57305	AAH57305 Sugar bee
37	554	75.3	8012	20	AAH57305	AAH57305 Sugar bee
38	554	75.3	8012	21	AAH57305	AAH57305 Sugar bee
39	554	75.3	8012	22	AAH57305	AAH57305 Sugar bee
40	554	75.3	8012	23	AAH57305	AAH57305 Sugar bee
41	554	75.3	8012	24	AAH57305	AAH57305 Sugar bee
42	554	75.3	8012	25	AAH57305	AAH57305 Sugar bee
43	554	75.3	8012	26	AAH57305	AAH57305 Sugar bee
44	554	75.3	8012	27	AAH57305	AAH57305 Sugar bee
45	554	75.3	8012	28	AAH57305	AAH57305 Sugar bee

#### ALIGNMENTS

RESULT 1  
ID ABSS3103 standard; DNA; 736 BP.  
AC ABSS3103;  
DN 29-NOV-2002 (first entry)  
KW Transgene expression related bidirectional dual promoter complex #1.  
KW Bidirectional dual promoter complex; transfection; transgene;  
KW agronomic performance; transformation; ds.  
OS Synthetic.  
FH Key  
FT msec\_feature 1. 736  
FT /tag a  
FT /note: The complement of this sequence is also claimed  
PN in claim 9 as SEQ ID number 2.  
XX NO200264804-A2.  
XX 22-AUG-2002.  
XX 11-FEB-2002; 2002MO-US004188.  
XX 11-FEB-2001; 2001US-0268358P.  
XX (WFL) UNIV FLORIDA.  
XX L1 Z, Gray DJ;  
XX WFL, 2002-627601/67.  
XX New bi-directional promoter complex comprising a modified enhancer region  
XX including at least 2 enhancer sequences, and at least 2 core promoters,  
XX useful for enhancing or improving transcriptional activity of transgenes.  
XX Claim 9, Fig 2; 77pp; English.  
XX

CC The invention describes a bi-directional promoter complex comprising a  
CC modified enhancer region that includes at least 2 enhancer sequences, and  
CC at least 2 core promoters. The core promoters are on either side of the  
CC modified enhancer region in a divergent orientation. The bi-directional  
CC promoter complex is useful for enhancing transcriptional activity of  
CC genes in transgenic plants. The promoter complex includes a bi-directional  
CC promoter complex with plants. Vectors that include the bi-directional  
CC promoter complex may be used to express foreign genes in mammalian cells  
CC and in plant cells including dicots and monocots. This sequence  
CC represents a bidirectional dual promoter complex useful for enhancing  
CC transcriptional activity of transgenes  
XX  
XX  
SQ Sequence 736 BP; 222 A; 176 C; 175 G; 163 T; 0 U; 0 Other;  
Query Match 99.8%; Score 734.4; DB 6; Length 736;  
Best Local Similarity 99.8%; Pred. No. 8.1e-232; Indels 0; Gaps 0;  
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATCCAGCTGCTCTCCCAATGAATGAATCTCTTATATAGAGAGGGTCTTGG 60  
DB 1 GGATCCAGCTGCTCTCCCAATGAATGAATCTCTTATATAGAGAGGGTCTTGG 60  
QY 61 AAGGATAGTGGATTTGGCTCATCTCTTACGTGAGTGGAGATCTCGAGAAGCTTCTGC 120  
DB 61 AAGGATAGTGGATTTGGCTCATCTCTTACGTGAGTGGAGATCTCGAGAAGCTTCTGC 120  
QY 121 AGTGAGCTTTTCAAGAGGGTATATCGGAACTCTCTCGAGTTCATTCGAGCT 180  
DB 121 AGTGAGCTTTTCAAGAGGGTATATCGGAACTCTCTCGAGTTCATTCGAGCT 180  
QY 181 ATCTGTCACTTATCAAGAGGAGTATAGAGAGGGTGGCACTTACAAATGGCATAT 240  
DB 181 ATCTGTCACTTATCAAGAGGAGTATAGAGAGGGTGGCACTTACAAATGGCATAT 240  
QY 241 TGGGATTAAGAGAGGGTATGTTCAAGATGCTCTCGCAGTGGTCCCAAGATGGA 300  
DB 241 TGGGATTAAGAGAGGGTATGTTCAAGATGCTCTCGCAGTGGTCCCAAGATGGA 300  
QY 301 CCCCACCCACGAGGAGCATCTGGGAAAGAGAGCGTTCCACACAGCTTCTTAAGCA 360  
DB 301 CCCCACCCACGAGGAGCATCTGGGAAAGAGAGCGTTCCACACAGCTTCTTAAGCA 360  
QY 361 GTGAGTATGATGATTCGATGAGCACTTTTCAAGAGGGTATATCGGAAAGCTCTC 420  
DB 361 GTGAGTATGATGATTCGATGAGCACTTTTCAAGAGGGTATATCGGAAAGCTCTC 420  
QY 421 GGATTCATTCGCGAGTATCTGTCACTTATCAAGAGGAGTATAGAGAGGGTGGC 480  
DB 421 GGATTCATTCGCGAGTATCTGTCACTTATCAAGAGGAGTATAGAGAGGGTGGC 480  
QY 481 ACCTCAATGCTCATCTGATTAAGAGAGGGTATGATGATGATGATGATGATGATG 540  
DB 481 ACCTCAATGCTCATCTGATTAAGAGAGGGTATGATGATGATGATGATGATGATG 540  
QY 541 AGTGGTCCCAAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATG 600  
DB 541 AGTGGTCCCAAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATG 600  
QY 601 ACCACAGCTCTTCAAGAGTGGATGATGATGATGATGATGATGATGATGATGATG 660  
DB 601 ACCACAGCTCTTCAAGAGTGGATGATGATGATGATGATGATGATGATGATGATG 660  
QY 661 CAATGCCATCTCTTGGAGAGGGTCTCTCTATATAGAGAGTTCATTCATTTGGAG 720  
DB 661 CAATGCCATCTCTTGGAGAGGGTCTCTCTATATAGAGAGTTCATTCATTTGGAG 720  
QY 721 AGGACAGCTGGATCC 736  
DB 721 AGGACAGCTGGATCC 736

ID ABS53105 standard; DNA; 1360 BP.  
XX  
XX ABS53105;  
XX  
XX 29-NOV-2002 (first entry)  
DT  
DE Transgene expression related bidirectional dual promoter complex #2.  
XX  
XX Bidirectional dual promoter complex; transgene;  
KW agronomic performance; transformation; ds.  
XX  
XX Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
XX misc\_feature 7..1360  
XX FT  
XX FT /note="The complement of this sequence is also claimed  
XX FT in claim 10 as SEQ ID number 4"  
XX  
XX WO200264804-A2.  
XX  
XX 22-AUG-2002.  
XX  
XX 13-FEB-2002; 2002WO-US004188.  
XX  
XX 13-FEB-2001; 2001US-0269359P.  
XX (UYFL) UNIV FLORIDA.  
XX  
XX Li Z, Gray DJ;  
XX  
XX MPI; 2002-627601/67.  
XX  
XX New bi-directional promoter complex comprising a modified enhancer region  
XX including at least 2 enhancer sequences, and at least 2 core promoters,  
XX useful for enhancing or improving transcriptional activity of transgenes.  
XX  
XX Claim 10; Fig 4; 77pp; English.  
XX  
XX The invention describes a bi-directional promoter complex comprising a  
XX modified enhancer region that includes at least 2 enhancer sequences, and  
XX at least 2 core promoters. The core promoters are on either side of the  
XX modified enhancer region in a divergent orientation. The bi-directional  
XX promoter complex is useful for enhancing transcriptional activity of  
XX transgenes to improve agronomic performance used in genetic  
XX transformation with plants. Vectors that include the bi-directional  
XX promoter complex may be used to express foreign genes in mammalian cells  
XX and in plant cells including dicots and monocots. This sequence  
XX represents a bidirectional dual promoter complex useful for enhancing  
XX transcriptional activity of transgenes  
XX  
XX Sequence 1360 BP; 353 A; 319 C; 317 G; 371 T; 0 U; 0 Other;  
Query Match 81.2%; Score 597.4; DB 6; Length 1360;  
Best Local Similarity 99.8%; Pred. No. 2.2e-186;  
Matches 598; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 109 AGAGCTTCTCGAGTGGAGCTTTTCAAGAGGGTATATCGGAAACCTCTCGGATTC 168  
DB 762 ATAGCTTCTCGAGTGGAGCTTTTCAAGAGGGTATATCGGAAACCTCTCGGATTC 821  
QY 169 CATTCGCGAGTATCTGTCTCATCAAGAGGAGTATAGAGAGGGTGGACCTTAC 228  
DB 822 CATTCGCGAGTATCTGTCTCATCAAGAGGAGTATAGAGAGGGTGGACCTTAC 881  
QY 229 AATTCGCTCATTCGAGTAAAGAGGGTATCTTCAAGATGCTCTCGGACAGTGGT 288  
DB 882 AATTCGCTCATTCGAGTAAAGAGGGTATCTTCAAGATGCTCTCGGACAGTGGT 941  
QY 289 CCAAGAGTGAACCCCAACCCAGGAGCATCTGCGAAAGAGAGAGAGAGAGAGAGAG 348  
DB 942 CCAAGAGTGAACCCCAACCCAGGAGCATCTGCGAAAGAGAGAGAGAGAGAGAGAG 1001

CC	expression of the promoter. It was excised as a ClaI-HindIII fragment,	
CC	induced with 100 µM p01 and inserted into the HindII site of	
CC	pUC19. The upstream region was excised from the HindIII	
CC	plasmid as a HindIII-BspEI fragment (3,343 to 3,420)	
CC	cloned into the HindIII and PstI sites. The enhanced	
CC	thus contains a duplication of sequences -343 to -90. See also	
CC	NC81003	
XX	Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;	
XX		
XX	Query Match 75.3%; Score 554; DB 1; Length 661;	
XX	Best Local Similarity 94.5%; Pred. No. 3,44-172;	
XX	Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1	
QY	116 TCGCATGAGATGATCTTCAAGAGGCTAATACGGGAACTCTCGGATTCATTGCC 175	
DB	20 TCGATGTGAGACTTTTCAAGAGGCTAATACGGGAACTCTCGGATTCATTGCC 79	
QY	176 CAGCATCTGTGCACTTATCAAAAAGACAGTGAAGAAAGAAAGTGCATCTCAACATCC 225	
DB	140 ATCATGCGATTAAAGAAAGGCGCATCTGTGAAGATCTCTGCGACAGATGTGCCAAG 189	
QY	236 ATCATTCGATTAAAGAAAGGCTATCTTCAAGATGCTCTGCGACAGATGTGCCAAG 285	
DB	80 CAGCATCTGTGCACTTATTTGAAAGATGATGAAAGAAAGAGTGTGCTTCAAAATCC 139	
QY	286 ATGACACCCCAACCGACGAGCATCTGTGAAAGAAAGAGGTTCCACACGCTTCAA 355	
DB	200 ATGACACCCCAACCGAGGCACTGTGAAAGAAAGAGGTTCCACACGCTTCAA 289	
QY	356 AGCAAGGAGATGATGATGAT---TGCATGAGACTTTTCAAAAGGATATATCGGA 411	
DB	260 AGCAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 319	
QY	412 AACCTCTCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 471	
DB	330 AACCTCTCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 379	
QY	472 GAGGTGCGACCTTCAAAATGCGATCTTCGATTAAAGAAAGGCTATCTTCAAGTCC 531	
DB	380 GAGGTGCGACCTTCAAAATGCGATCTTCGATTAAAGAAAGGCTATCTTCAAGTCC 439	
QY	532 TCGGCGAGAGGATGTCGAAAGATGACCCCGACGACGAGAGATCTGTGAAAGAAAG 491	
DB	440 TCGGCGAGAGGATGTCGAAAGATGACCCCGACGAGAGATCTGTGAAAGAAAG 491	
QY	592 GAGGTGCGACAGAGCTTCAAGAGAGGATGATGATGATGATGATGATGATGATGATG 651	
DB	500 GAGGTGCGACAGAGCTTCAAGAGAGGATGATGATGATGATGATGATGATGATGATG 559	
QY	652 GATGAGCGACATTCGATTCCTTGGCAGAGCCCTCTCTTAAAGAAAGTTCAATT 711	
DB	560 GATGAGCGACATTCGATTCCTTGGCAGAGCCCTCTCTTAAAGAAAGTTCAATT 619	
QY	712 CATTTGAGAGAGACAGGCTG 731	
DB	620 CATTTGAGAGAGACAGGCTG 639	
XX		
XX	RESULT 4	
XX	AA991710	
XX	AA991710 standard; DNA, 661 BP.	
XX	AA991710;	
XX	25-MAR-2003 (rev'ed)	
XX	12-MAR-1990 (first entry)	
XX	Enhanced CMV35 promoter used in plasmid pMON893.	
XX	CMV35S promoter; Bacillus thuringiensis; toxin protein; insecticide;	
XX	plasmid pMON893.	

OS Cauliflower mosaic virus.  
 XX Key Location/Qualifiers  
 FT misc\_feature 27..279  
 FT /tag= a  
 FT /note= "duplicated enhancer sequence"  
 FT misc\_feature 289..541  
 FT /tag= b  
 FT /note= "duplicated enhancer sequence"  
 XX EP339009-A.  
 XX 25-OCT-1989.  
 XX 14-APR-1989; 89EP-00870047.  
 XX 11-APR-1988; 8BUS-00179709.  
 XX (MONS ) MONSANTO CO.  
 XX Fuchs RL, Kishore GM, Macintosh SC;  
 XX WPI; 1989-311431/43.  
 XX Toxin protein of *Bacillus thuringiensis* bacteria - improved in efficacy  
 XX using a potentiating amt. of a trypsin inhibitor.  
 XX Disclousure; Fig 14; 56pp; English.  
 XX A fragment of the *CaMV35S* promoter (-343 to +9) in pUC13 was excised as a  
 CC ClaI-HindIII fragment and blunt-ended. This was inserted into the HindIII  
 CC site of pUC18. The upstream region of the 35S promoter was excised as a  
 CC HindIII-EcoRV fragment (extending from -343 to -90) and inserted into the  
 CC same plasmid between the HindIII and PstI sites. The enhanced promoter  
 CC thus contains a duplication of sequences between -343 and -90. The  
 CC promoter is used in plasmid pMON93 to express *Bacillus thuringiensis*  
 CC toxin with a potentiating amt. of a trypsin inhibitor. This is useful as  
 CC an insecticide. (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;  
 SQ

Query Match 75.3%; Score 554; DB 1; Length 661;  
 Best Local Similarity 94.5%; Pred. No. 3.4e-172;  
 Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

QY 116 TCTCGAGTGAAGCTTTTCAACAAAGAGGTAATATCGGAAACCTCTCGGATTCATTCGCC 175  
 DB |||  
 QY 176 GAGCTATCTGTCTCTCTCAAAAGGACGCTAGAAAGAGAGCTGCGCTCAAAATGCC 235  
 DB |||  
 QY 236 ATCATTCGATAAAGAAAGGCTATCTGTCAGATGCTCTGCGGACAGTGTGCCAAAG 295  
 DB |||  
 QY 140 ATCATTCGATAAAGAAAGGCTATCTGTCAGATGCTCTGCGGACAGTGTGCCAAAG 199  
 QY 296 ATGAGACCCCAACCAAGAGGATCGTGGAAAGGAGAGCTTCCAAACCAAGCTTCCAA 355  
 DB |||  
 QY 200 ATGAGACCCCAACCAAGAGGATCGTGGAAAGGAGAGCTTCCAAACCAAGCTTCCAA 259  
 QY 356 AGCAAGTGAATGATGAT-TCAGTGAAGCTTCAAGAGGATTAATTCGGA 411  
 DB |||  
 QY 260 AGCAAGTGAATGATGATGCTGCAAGTGAAGCTTCAAGAGGATTAATTCGGA 319  
 QY 412 AACCTCTCGATTCATTCGCAAGCTATCTGTCACATCATCAAAAGAGAGTGAAGAAG 471  
 DB |||  
 QY 320 AACCTCTCGATTCATTCGCAAGCTATCTGTCACATCATCAAGAGATGAGGAAG 379  
 QY 472 GAAGGTGGACCTACAAATGCCATTCGCAAGAGAGGATTCGTCAGATGCC 531  
 DB |||  
 QY 380 GAAGGTGGCTCTCAAAATGCCATTCGCAAGAGAGGCTATGTCAGATGCC 439

QY 532 TCTCGAGTGAAGCTTTTCAACAAAGAGGTAATATCGGAAACCTCTCGGATTCATTCGCC 591  
 DB |||  
 QY 440 TCTCGAGTGAAGCTTTTCAACAAAGAGGTAATATCGGAAACCTCTCGGATTCATTCGCC 499  
 QY 592 GACGTTCACACACCTCTTCAAGCAAGTGGATTTGATGATATCTCCACTGACCTAAGG 651  
 DB |||  
 QY 500 GACGTTCACACACCTCTTCAAGCAAGTGGATTTGATGATATCTCCACTGACCTAAGG 559  
 QY 652 GATGAGCACAATCCCACTATCTTCCGAAGACCTTCTCTCTATATAAGGAAGTTTCATT 711  
 DB |||  
 QY 560 GATGAGCACAATCCCACTATCTTCCGAAGACCTTCTCTCTATATAAGGAAGTTTCATT 619  
 QY 712 CATTTGAGAGGAGAGCTG 731  
 DB |||  
 QY 620 CATTTGAGAGGAGAGCTG 639

RESULT 5  
 AAD01017  
 ID AAD01017 standard; DNA; 2107 BP.  
 AC AAD01017;  
 XX 21-SEP-2000 (first entry)  
 XX Expression cassette-4 comprising modified E. coli P2A phnO coding gene.  
 XX Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT;  
 XX acyltransferase; transacylase; recombinant plant; expression cassette;  
 XX corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide;  
 XX CTP; glyphosate oxidase; GOM; glyphosate oxidoreductase; phnO gene;  
 XX self-fertilization; hetero-fertilization; ds.  
 XX *Escherichia coli*.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Promoter /tag= a  
 FT 5'UTR /note= "Plant functional heterologous promoter"  
 FT /tag= b  
 FT Intron /note= "Enhances expression of the phnO gene"  
 FT /tag= c  
 FT transit\_peptide /note= "Enhances expression of the phnO gene"  
 FT /tag= d  
 FT CDS /note= "Targets the protein to an intracellular  
 1427..1861  
 /tag= e  
 FT /product= "Escherichia coli modified P2A AMPA  
 acyltransferase (AAT) enzyme"  
 FT /function= "Transfers acyl group from an acylcarrier  
 (CoA) to the free amino group of aminomethylphosphonate"  
 FT terminator 1869..2102  
 /tag= f  
 FT WO200029596-A1.  
 XX 25-MAY-2000.  
 XX 16-NOV-1999; 99WO-US027152.  
 XX 17-NOV-1998; 98US-0108763P.  
 XX (MONS ) MONSANTO CO.  
 XX Barry GF;  
 XX WPI; 2000-387806/33.  
 XX P-PSDB; AMY1251.







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QY 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGGTGGCACTCAAAATGCC 235
DB |||||||
QY 236 ATGATTTGCGATTAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGTGCCAAG 295
DB |||||||
QY 148 ATGATTTGCGATTAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGTGCCAAG 207
DB |||||||
QY 296 ATGATTTGCGATTAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGTGCCAAG 355
DB |||||||
QY 208 ATGATTTGCGATTAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGTGCCAAG 267
DB |||||||
QY 356 AGCAAGTGGATGATGTGAT-----TGCAGTGGAGCTTTTCAAGAAAGGTAATATCGGA 411
DB |||||||
QY 268 AGCAAGTGGATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 337
DB |||||||
QY 412 AACCTCTCGGATTCGATTCGCGAGGATTCGATTCGATTCGATTCGATTCGATTCGATTC 471
DB |||||||
QY 328 AACCTCTCGGATTCGATTCGCGAGGATTCGATTCGATTCGATTCGATTCGATTCGATTC 387
DB |||||||
QY 472 GAAGTGGACCTCAAAATGCGATCATTTGGATTAAGGAAAGGCTATCGTTCAAGATGCC 531
DB |||||||
QY 388 GAAGTGGCTCTCTCAAAATGCGATCATTTGGATTAAGGAAAGGCTATCGTTCAAGATGCC 447
DB |||||||
QY 532 TGTGCGACAGTGTGCTCCAAAGATGAGACCCCAACCAAGAGGAGATCGTGGAAAGAA 591
DB |||||||
QY 448 TGTGCGACAGTGTGCTCCAAAGATGAGACCCCAACCAAGAGGAGATCGTGGAAAGAA 507
DB |||||||
QY 592 GAGTGTCCACAGCTCTTCAAGCAAGTGTGATGATGATGATGATGATGATGATGATGATG 651
DB |||||||
QY 508 GAGTGTCCACAGCTCTTCAAGCAAGTGTGATGATGATGATGATGATGATGATGATGATG 567
DB |||||||
QY 652 GATGAGCAGCAATCCACTATCTTCCGACAGCTCTTCCATATAGGAGTTCATTT 711
DB |||||||
QY 568 GATGAGCAGCAATCCACTATCTTCCGACAGCTCTTCCATATAGGAGTTCATTT 627
DB |||||||
QY 712 CATTTGGAGAGACACCGCTG 731
DB |||||||
QY 628 CATTTGGAGAGACACCGCTG 647
DB |||||||

RESULT 8
ID AEP22504 standard; DNA; 2767 BP.
AC AEP22504;
XX
DT 23-MAR-2006 (first entry)
XX
DE RNAi transcription unit with polyadenylation site vector 1A.
XX
KW de; gene; Hsp70; heat shock protein 70; luciferase; nopaline synthase;
KW transgenic plant; RNA interference; gene silencing; pathogen resistance;
KW plant pest; plant growth regulant; insect resistance; crop improvement.
XX
OS Cauliflower mosaic virus.
OS Zea mays.
OS Agrobacterium tumefaciens.
OS Chimeric.
XX
PH Key
FT Location/Qualifiers
FT 1..614
FT /*tag= a
FT /*label= CaMV_35S
FT 645..1448
FT /*tag= b
FT /*label= Zea_mays_Pe35S-Hsp_intron
FT repeat_region
FT 1025..2502
FT /*tag= d
FT /*label= INVERTED
FT complement(1025..1455)
FT CDS
FT /*tag= c

```

```

FT /*product= "Firefly luciferase (LUC)"
FT /*note= "No start or stop codons shown"
FT /*partial
FT 2082..2502
FT /*tag= e
FT /*product= "Firefly luciferase (LUC)"
FT /*partial
FT /*note= "No start or stop codons shown"
FT 2515..2767
FT /*tag= f
FT /*note= "From Agrobacterium tumefaciens nopaline synthase
FT gene"
XX US2006026711-A1.
XX
XX 03-FEB-2006.
XX
XX 20-JUL-2005; 2005US-00186196.
XX 21-JUL-2004; 2004US-0589643P.
XX
XX (HUAN/) HUANG S.
XX (GILB/) GILBERTSON L A.
XX
XX Huang S, Gilbertson LA;
XX WPI; 2006-124885/13.
XX
XX
XX Non-sytemic gene suppression comprises transcribing in a transgenic
XX plant a recombinant DNA construct comprising a promoter operably linked
XX to a gene suppression element.
XX
XX Example 1; SEQ ID NO 1; 12pp; English.
XX
XX The present sequence is that of a synthetic vector produced in the
XX invention of a novel method for the non-sytemic suppression of a
XX target gene consisting of a recombinant DNA construct comprising a
XX DNA construct consisting of a promoter operably linked to a gene
XX suppression element, producing RNA that non-sytemically suppresses a
XX target gene and is retained in the nucleus, therefore suppressing the
XX target gene relative to expression in the absence of the transcription.
XX The RNAi transcriptional unit of vector 1A included (a) a chimeric
XX promoter including an enhanced CaMV35S promoter linked to an enhancer
XX element (the maize Pe35S-Hsp intron), (b) an inverted repeat of DNA
XX coding for firefly luciferase with anti-sense oriented DNA followed by a
XX sense oriented DNA and (c) a 3'UTR DNA from Agrobacterium tumefaciens
XX nopaline synthase gene which provides a polyadenylation site. Vector 1A
XX and Renilla luciferase gene which provides a polyadenylation site.
XX Suppression experiments were performed to confirm the efficacy of the
XX for gene suppression exhibited by constructs without a functional
XX polyadenylation site relative to those with. A target gene is a gene
XX native to the transgenic plant, a transgene in the transgenic plant, a
XX gene native to a pest or pathogen of the transgenic plant, or a microRNA
XX precursor DNA sequence. The promoter is a seed-specific promoter and the
XX non-sytemic suppression is seed-specific suppression of a target gene.
XX The invention is useful for crop resistance to a pest or pathogen where
XX the pest is an insect, e.g. a coleopteran, or a nematode, where the
XX nematode is a root nematode and the tissue-specific promoter is a root-
XX specific promoter.
XX
XX Sequence 2767 BP; 774 A; 569 C; 580 G; 844 T; 0 U; 0 Other;
XX
XX Query Match 75.3%; Score 554; DB 15; Length 2767;
XX Best Local Similarity 94.5%; Pred. No. 6.8e-172;
XX Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
XX
XX QY 116 TTCGAGTGAAGCTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCCTATGCC 175
XX |||||||
XX 3 TCCGATGTGAGCTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCCTATGCC 62
XX |||||||
XX 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGGTGGCACTCAAAATGCC 235.
XX |||||||

```

[illegible]

	CDS	1241..3302	/transg=d
FT	FT	/transg=	"Cry3B variant 112jimv2"
PT	terminator	/product=	3217..3450
FT	FT	/transg=g	
FT	FT	/label=p-TA-hsp17	
FT	FT	/note= wheat heat shock hsp17 transcription termination	
XX	XX	/and polyadenylation sequence"	
FN	Moz00011185-AZ.		
PD	02-MAR-2000.		
PD	19-AUG-1999.	99WO-US018883.	
PR	19-AUG-1998.	98US-0097150P.	
PR	(MONS ) MONSANTO CO.		
PI	Romano CP;		
DR	WPI; 2000-246568/21.		
DR	P-P5DB; AAY0446.		
PF	Novel expression cassette which express Bacillus thuringiensis Cry3		
PF	delta-endotoxin portion which is toxic to coleopteran insect pests,		
PP	useful for producing transgenic plants with improved insecticidal		
XX	activity.		
PS	Claim 16; Page 149-152; 17dp; English.		
XX	The present sequence is an expression cassette from a Cry3B plant		
CC	expression vector pMON31748. It comprises an enhanced Cauliflower mosaic		
CC	virus (CaMV) 35S promoter sequence, a wheat chlorophyll A/B binding		
CC	protein untranslated leader sequence, a rice actin intron segment, a		
CC	Bacillus thuringiensis delta-endotoxin coding sequence, and a poly(A)		
CC	polydenylation sequence. This expression cassette is used to improve		
CC	expression of Cry3B variant protein in transgenic plants e.g. maize, to		
CC	increase insecticidal activity against Coleopteran pests. (Updated on 15-		
SQ	SEP-2003 to standardise OS field)		
XX	Sequence 3469 BP; 790 A; 1078 G; 845 G; 756 T; 0 U; 0 Other;		
Query Match	75.3%; Score 554; DB 3; Length 3469;		
Bacc Local Similarity	34.3%; Pctid No: 7; ee -172; Mismatches 36;		
Matches	Conservative 0; Mismatches 30; Indels 4; Gaps 1		
Oy	116 CACGACTCTGTCAATTCATCAAAGAAAGCAAGTGAAGAAGAGTGTCACCTCAAAATGCC	235	
Dd	28 TCAGATGGAGCATTTTCCAACAAGGTAATACTCGGAATCCCTCGGATTGCATTTGCC	87	
Oy	176 CAGCTATCTGTCAATTCATCAAAGCAAGTGAAGAAGAGTGTCACCTCAAAATGCC	235	
Dd	88 CAGCTATCTGTCAATTCATGTGAAGATAGTAGAAAAAGATGAGCTCTCAAAAATGCC	147	
Oy	235 ATCTATGGCATAAAGAAAGGCTATACGTCAAGATGCTCTGGCCAGAGTGTCCTCAAG	295	
Dd	148 ATCAATTCGATAAAGAAAGGCCCATCTGTGAAGATGCTCTGGCCACAGTGATCCCAAG	207	
Oy	296 ATGAGACCCCCAACAGAGAGATCTGTGAAAAAAGAAAGATTCACCAAGCTTTCA	355	
Oy	208 ATGAGACCCCCAACAGAGAGATCTGTGAAAAAAGAAAGATTCACCAAGCTTTCA	267	
Dd	356 AGCAATGATATGATNGT-----TGCATGATGCACTTTCAADAAGGTAATGCCGA	411	
Oy	266 AACGATCTCGGATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT	327	
Oy	412 AACGATCTCGGATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT	471	
Dd	328 AACGATCTCGGATATTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT	387	
Oy	472 GAAGGTGACCCTCAAAATGCGCATCTTGCGATAAAGAAAGGCTATGCTTCAGATGCC	531	



[illegible]

CC	pathogenesis is achieved using the modified polynucleotide. The modified
CC	polynucleotide reduces the number of transgene events that have to be
CC	screened in order to identify one which contains beneficial levels of one
CC	or more insect controlling compositions or proteins present at a desired level.
CC	In some embodiments, the insecticidal polynucleotide is expressed as a
CC	cassette #2 DNA.
SQ	Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;
Query Match	75.3%; Score 554; DB 10; Length 3469;
Best Local Similarity	94.5%; Prid. No. 7.6e-172;
Matches 586;	Conservative 0; Mismatches 30; Indels 4; Gaps 1
Dy	116 TCCTGATGAGACCTTTTCAAAACGGTAATTCGGAACCTCTCGGTATTCATTGGC 175
Oy	176 CACTCATCTGTCACTTCATCAAAGAAGTAGTAAAAGAGGTGGACCTCAAAATGCC 235
Dy	88 CACATACGTGCATCTTATGTGTAAAGATGTGAAAAGAAAGTGCTCTCAAAATGCC 147
Oy	236 ATCATTCGATTAAGAAAGAGCTATTCCTTCAAGATGCTCTTGGCCAGATGTCTCCAG 295
Dy	148 ATCATTCGATTAAGAAAGAGCTATTCGTGAAGATGCTCTTGGCCAGATGTCTCCAG 207
Oy	236 ATGAGACCCCACCCAGAGAGATTCGTGAAAAAAGAGAGTTCACAACACGCTTCCA 355
Dy	208 ATGACACCCACCCAGAGAGATTCGTGAAAAAAGAGAGTTCACAACACGCTTCCA 267
Oy	356 AGCAAGGTGATGATGTGAT---TGCGATGAGACTTTTCACAAGAGGTAAATATCGGGA 411
Dy	268 AGCAAGGTGATGATGATGTGATGTGCGATGAGACTTTTCACAAGAGGTAAATATCGGGA 327
Oy	412 AACCTCTGGAATTCATATGCGCCAGCTATTCCTGATCTCAAAAGACAGTAGAAG 471
Dy	328 TAAGCTCTGGAATTCATATGCGCCAGCTATTCCTGATCTCAAAAGACAGTAGAAG 387
Oy	472 GAAGTGTGGACCTCAAAATGCGATCATATGTGATAAGAAAGAGCTATGTGTCAATGCC 533
Dy	388 GAAGTGTGCTCTCAAAATGCGATCATATGTGATAAGAAAGAGAGCTATGTGTCAATGCC 447
Oy	532 TCTGCGACAGATGTGCTCCMAAGATGGAACCCCAACCAAGAGAGCATGTGTGAAAAAGA 591
Dy	448 TCTGCGACAGATGTGCTCCMAAGATGGAACCCCAACCAAGAGAGCATGTGTGAAAAAGA 507
Oy	592 GAGGTTCGACACCGTCTTCAAGAGAGTGAATGTGAATATTCACATGACGTAAGG 651
Dy	508 GAGGTTCGACACCGTCTTCAAGAGAGTGAATGTGAATATTCACATGACGTAAGG 567
Oy	652 GATGAGCGCAATCCCAATACCTGTGCGAAGACCCTCTCTATATAGAGAAATTCATT 711
Dy	568 GATGAGCGCAATCCCAATACCTGTGCGAAGACCCTCTCTATATAGAGAAATTCATT 627
Oy	712 CATTTGAGAGAGACAGCTG 721
Dy	628 CATTTGAGAGAGACAGCTG 647
RESULT 12	
AEB66524	
ID	AEB66524 standard; DNA; 3469 BP.
NC	AEB66524;
XX	09-FEB-2006 (first entry)
DE	Bt cry3Bb.11231mw2 expression vector DNA, pMON31748.
XX	crop improvement; transgenic plant; insect resistance; gene expression;
KM	Coleopteran inhibitory activity; insecticide; endotoxin; Cry3Bb; gene;
KM	ds; circular; vector; gene fusion; promoter; heat shock protein; intron;
XX	chlorophyll A/b binding protein; actin.



FT		/tag= b
FT		/label= 1-6m_Hep70
FT		/note= *see mya Hep70 intron sequence"
PT	CDS	1490..3451
FT		-tag= c
FT		/product= "Cry3Bb variant AAV1231"
FT	terminator	3473..3730
PT		/tag= T-GRU nos
FT		/label= 1-AGRU nos
FT		/note= "Agrobacterium tumefaciens nopaline synthase 3'
FT		transcription termination and polyadenylation sequence"
PX		WO20001185-A2.
PX		
PD	02-MAR-2000.	*
PD		
PP	19-AUG-1999,	99MC-US018083.
PK	19-AUG-1998;	98US-0097150P.
XX	(MONS ) MONSANTO CO.	
PA	Romano CP;	
PI	WP1; 2000-246568/21.	
DR	P-ESDB; AAV70444.	
PS		
XX		
XX		
PS	Claim 16; Page 125-128; 171pp; English.	
XX		
XX	The present sequence is an expression cassette from a Cry3Bb plant	
CC	expression vector pKMON3J710. It comprises an enhanced Cauliflower mosaic	
CC	virus (CaMV) 35S promoter sequence, a maize Hsp70 intron sequence, a	
CC	Bacterial Artificial Chromosome (BAC) clone containing the coding	
CC	sequence and a multiple synthesis transcription termination and coding	
CC	polyadenylation sequence. This expression cassette is used to improve	
CC	expression of Cry3B variant protein in transgenic plants e.g. maize, to	
CC	increase insecticidal activity against coleopteran pests. Updated on 15-	
CC	SEP-2003 to standardise OS field)	
SQ	Sequence 3754 BP; 1030 A; 889 G; 800 G; 1035 T; 0 U; 0 Other;	
Query Match	75.3%; Score 554; DB 3; Length 3754;	
Seq. Id. Similarity	34.5%; Ident No. 7; 9e-172;	
Matches	356; Conservative 0; Mismatches 30; Indels 4; Gaps 1	
Oy	116 TCCTGCAAGAGACTTTTTCACAAAGGGTAATATCGGAATCTTCGTGATTCATTCATTCGC	175
Dd	28 TCCCATGTGAGACTTTTTCACAAAGGGTAATATCGGAATCTTCGTGATTCATTCATTCGC	87
Oy	176 CACGATTATGTCATCTTCATCAAAGAGACATGTGAAAAGAGAGTGTCGACCTTCGAAATGCC	235
Dd	88 CACGATTATGTCATCTTCATCAAAGAGACATGTGAAAAGAGAGTGTCGACCTTCGAAATGCC	147
Oy	236 ATGATATGTGATTAAGAAGAGGCTAATCTTCAGATGCTCTGCGACAGTGTCTCCCAAG	225
Dd	148 ATGATATGTGATTAAGAAGAGGCTCTGTGAAATGCTCTTCCGACAGAGGTCTCCCAAG	207
Oy	236 ATGAGACCCCCACCGACGAGAGCATGTGTGAAAAAGAAAGAGATCCCAACAGCTTCGAA	355
Dd	208 ATGAGACCCCCACCGACGAGAGCATGTGTGAAAAAGAAAGAGATCCCAACAGCTTCGAA	267
Oy	356 AGCAGATGATTAATGTAT---TGCAGTAGACTTTTTCACAAAGGGTAATATCGGAA	411
Dd	268 AGCAGATGATTAATGTATGTATGTATGTCATGATGATGATTCATCAAAGAGACAGTGAAG	327
Oy	412 AACCTCTCGGATATTCATTCATTCGTCACATCTTCATCAAAGAGACAGTGAAG	471
Dd	328 AACCTCTCGGATATTCATTCGTCACATCTTCATCAAAGAGACAGTGAAG	387

QY	472	GAAAGTGGGACCTTACCAATTCCTCATATTCATTAAGGAAGGCTATCTTCAAGATGCC	53
Db	388	GAAAGTGGGCTCTTCAAAATTCCTCATATTCATTAAGGAAGGCTATCTTGAAGATGCC	447
QY	532	TCCTGCGACATGCTGTCTCCAAAGATGACCCCTCACGAGAGATCTGTGAAAAGAA	591
Db	448	TCCTGCGACAGAGGCTGTCCAAAGATGACCCCTCACGAGAGATCTGTGAAAAGAA	507
QY	592	GACGCTTCACCAACGCTCTTCAAGGAAGGATGATGATATCTCACTGAACGTAAAG	651
Db	508	GACGCTTCACCAACGCTCTTCAAGGAAGGATGATGATATCTCACTGAACGTAAAG	567
QY	652	GATGAGCCCAATCTCCCATCTCTCGCAAGACCTCTCTCATATTAAGAAAGTCAATT	711
Db	568	GATGAGCCCAATCTCCCATCTCTCGCAAGACCTCTCTCATATTAAGAAAGTCAATT	627
QY	712	CATTGGAGAGAACAGCTG 731	
Db	628	CATTGGAGAGAACAGCTG 647	
RESULT 14			
ID	AD661790		
AC	AD661790	standard; DNA; 3754 bp.	
XX	AD661790;		
DT	15-JUN-2004	(first entry)	
DE	Bt.cry3Bb.v11231	expression vector DNA, pMON33710.	
OS	Transgenic plant; Cry3Bb-delta-endotoxin; Coleopteran pest resistance;		
KM	insecticide; variant; cyclic; circular; chimeric; mate; gene; ds.		
XX	Chimeric - Cauliflower mosaic virus.		
OS	Chimeric - Zea mays.		
OS	Chimeric - Bacillus thuringiensis.		
OS	Chimeric - Agrobacterium tumefaciens.		
XX	Key	Location/Qualifiers	
FT	Promoter	25..640	
FT	FT	/*tag= "Cauliflower mosaic virus 35S promoter (p-	
FT	FT	CMV35S)"	
FT	intron	659..1472	
FT	FT	/*tag= b	
FT	FT	1490..3451	
FT	CDS	/*tag= c	
FT	FT	/*product= "Bt.cry3Bb.v11231 protein"	
FT	FT	misc_feature	
FT	FT	3475..3730	
FT	FT	/*tag= d	
FT	FT	/*note= "Agrobacterium tumefaciens nopaline synthase	
FT	FT	transcription termination and polyadenylation sequence (T	
FT	FT	-AATC-nos)"	
PN	US2003115630-A1.		
XX	19-JUN-2003.		
XX	29-AUG-2002; 2002US-00232665.		
XX	19-AUG-1999; 99US-00377466.		
XX	(ROMA/) ROMANO C P.		
XX	Romano CP.		
XX	WPI; 2003-810928/76.		
DR	P-PSDB; ABM01053.		
XX	New transgenic plant resistant to Coleopteran pests, comprises Bacillus		

New transgenic plant resistant to Coleopterian pests, comprises *Bacillus*

```

PT Thuringiensis Cry3-delta-endotoxin gene.
XX Claim 16; Page 57-60; Opp; English.
XX
CC The invention relates to novel transgenic plants comprising Bacillus
CC Thuringiensis Cry3-delta-endotoxin gene or its variants having
CC Coleopteran inhibitory activity. The invention is useful for controlling
CC Coleopteran pests in a field of crop plants. The present
CC sequence is a B. thuringiensis Cry3Bb-delta-endotoxin variant expression
CC vector DNA.
XX
SQ Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;
Query Match 75.3%; Score 554; DB 10; Length 3754;
Best Local Similarity 94.5%; Pred. No. 7.9e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
QY 116 TCTCGTGTGAGCTTTCACGAAAGGATATTCGGAAGCTCTTCGGATTCGATGCC 175
DB 116 TCTCGTGTGAGCTTTCACGAAAGGATATTCGGAAGCTCTTCGGATTCGATGCC 87
QY 176 CAGCTATGTGTCACTTCATCAAAAGGACAGTAGAAGAGGAGTGGCACTCAAAATGCC 235
DB 176 CAGCTATGTGTCACTTCATCAAAAGGACAGTAGAAGAGGAGTGGCACTCAAAATGCC 147
QY 236 ATCATTTGGATTAAGGAAAGGCTATCGTTCAAGATGCTTCCGACAGTGTGCCAAAG 295
DB 236 ATCATTTGGATTAAGGAAAGGCTATCGTTCAAGATGCTTCCGACAGTGTGCCAAAG 207
QY 296 ATGAGCCGCGACCCGACGAGGCTGTGGAAGAGAGAGGTTCCACACGCTTCAA 355
DB 296 ATGAGCCGCGACCCGACGAGGCTGTGGAAGAGAGAGGTTCCACACGCTTCAA 267
QY 356 AGCAAGTGGATGATGTGAT-----TGCAGTGAGCTTTTCAAAAAGGTAATTCGGA 411
DB 356 AGCAAGTGGATGATGTGAT-----TGCAGTGAGCTTTTCAAAAAGGTAATTCGGA 327
QY 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAG 471
DB 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAG 387
QY 472 GAAGTGGACCTACAAATGGCATATTCGATAAGGAAAGGCTATCGTTCAAGATGCC 531
DB 472 GAAGTGGACCTACAAATGGCATATTCGATAAGGAAAGGCTATCGTTCAAGATGCC 447
QY 532 TCTGCGACAGCTGTCCTCAAGAGTGGACCCACCCACGAGGAGCATCTGGAAGAA 591
DB 532 TCTGCGACAGCTGTCCTCAAGAGTGGACCCACCCACGAGGAGCATCTGGAAGAA 507
QY 592 GACGTTCCACACGCTCTTCAAGCAAGTGGATGTGATATCTCACTGACCTGAAGG 651
DB 592 GACGTTCCACACGCTCTTCAAGCAAGTGGATGTGATATCTCACTGACCTGAAGG 567
QY 652 GATGACGCAATTCCTCACTATCTTCGACAGCCCTTCTCTATATAGGAAGTTCAATT 711
DB 652 GATGACGCAATTCCTCACTATCTTCGACAGCCCTTCTCTATATAGGAAGTTCAATT 627
QY 712 CATTGTGAGAGGACAGCTG 731
DB 712 CATTGTGAGAGGACAGCTG 647
RESULT 15
ID ABX95186
XX ABX95186 standard; DNA; 3754 BP.
XX
XX ABX95186;
XX
XX 12-JUN-2003 (first entry)
XX
DE B. Thuringiensis delta endotoxin Cry3Bbvl1231 expression cassette #2.
XX
XX Cry3Bbvl1231; ds; gene; delta-endotoxin; plant; transgenic; insecticide;

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```

KM crystal 3; Cry3; Coleopteran insect infestation; increased toxicity;
KM season long protection; beetle; maize; expression cassette.
XX
OS Bacillus thuringiensis.
OS Zea mays.
OS Agrobacterium tumefaciens.
OS Cauliflower mosaic virus.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Promoter 25..640
XX /tag= a
XX /note= "Enhanced CaMV35S promoter"
XX FT intron 669..1472
XX /tag= b
XX /number= 1
XX /cons_splice= (5'site:NO,3'site:NO)
XX FT CDS 1490..3451
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XX FT misc_signal 3475..3730
XX /tag= d
XX /note= "Agrobacterium tumefaciens nopaline synthase"
XX transcription terminator and polyadenylation sequence"
XX US6501009-B1.
XX
XX 31-DEC-2002.
XX
XX 19-AUG-1999; 99US-00377466.
XX
XX 19-AUG-1999; 99US-00377466.
XX (MONS ) MONSANTO TECHNOLOGY LLC.
XX Romano CP;
XX
XX WPI; 2003-352192/33.
XX P-PSDB; ABU09198.
XX
XX New modified polynucleotide useful for controlling Coleopteran insect
XX infestation in a field of crop plants encodes insecticidal crystal 3
XX Bacillus thuringiensis delta-endotoxin.
XX
XX Disclosure; Col 105-110; 107pp; English.
XX
XX The invention relates to a modified polynucleotide which encodes an
XX insecticidal crystal 3 (Cry3) Bacillus thuringiensis delta-endotoxin such
XX as Cry3Bb. The modified polynucleotide is useful for producing a
XX transformed cell, by introducing the modified polynucleotide into a cell
XX such as a plant cell (preferably a maize cell) or a microbial cell. The
XX modified polynucleotide is useful for producing a transformed maize plant
XX by introducing the modified polynucleotide into a maize plant cell,
XX selecting a transformed maize plant cell and regenerating a maize plant
XX from the transformed maize plant cell. A transgenic plant expressing the
XX insecticidal crystal 3 protein in a field of crop plants, thereby providing
XX a useful for producing transgenic plants expressing higher levels of the
XX insect controlling B. thuringiensis delta-endotoxin. The modified
XX polynucleotide provides up to 10 fold higher levels of insect controlling
XX delta-endotoxin relative to the highest levels obtained using prior
XX compositions. In particular, transgenic maize expressing higher levels of
XX the Cry3Bb protein designed to exhibit increased toxicity toward
XX Coleopteran pests deliver superior levels of insect protection and are
XX less likely to sponsor development of populations of target insects that
XX are resistant to the insecticidally active protein. Improved control of
XX susceptible target insect pests and season long protection from insect
XX pathogens is achieved using the modified polynucleotide. The modified
XX polynucleotide encodes a transgenic plant that have to be
XX produced in a field of crop plants which contain beneficial levels of one
XX or more insect controlling compositions. The present invention includes
XX Bacillus thuringiensis delta endotoxin Cry3Bbvl1231 expression cassettes

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**Tue Jun 6 08:26:39 2006**

us-10-075-105c-1.rng

Page 14

[illegible]

Search completed: June 5, 2006, 05:12:57  
Job time : 530 secs



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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 05:04:33 ; Search time 196 Seconds  
(Without alignments)  
7026.204 Million call updates/sec

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Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	554	75.3	661	3	US-09-027-998A-33
3	554	75.3	2107	3	US-09-043-692-33
4	554	75.3	2107	3	US-09-043-692-33
5	554	75.3	2107	3	US-09-043-692-33
6	554	75.3	2107	3	US-09-043-692-33
7	554	75.3	3469	3	US-09-043-692-33
8	554	75.3	3469	3	US-09-043-692-33
9	554	75.3	3754	3	US-09-043-692-33
10	554	75.3	3754	3	US-09-043-692-33
11	554	75.3	8012	3	US-09-043-692-33
12	554	75.3	8349	3	US-09-043-692-33
13	554	75.3	8418	3	US-09-043-692-33
14	554	75.3	8418	3	US-09-043-692-33
15	554	75.3	8798	3	US-09-043-692-33
16	554	75.3	8798	3	US-09-043-692-33
17	554	75.3	1030	2	US-09-043-692-33
18	554	75.3	1030	2	US-09-043-692-33
19	554	75.3	1196	3	US-09-043-692-33
20	554	75.3	1196	3	US-09-043-692-33
21	554	75.3	5897	3	US-09-043-692-33
22	554	75.3	5897	3	US-09-043-692-33
23	554	75.3	9335	3	US-09-043-692-33

Sequence 14, Appl  
Sequence 13, Appl  
Sequence 8, Appl  
Sequence 9, Appl  
Sequence 10, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 4, Appl  
Sequence 1, Appl  
Sequence 15, Appl  
Sequence 7, Appl  
Sequence 8, Appl  
Sequence 9, Appl  
Sequence 30, Appl  
Sequence 30, Appl  
Sequence 30, Appl

24 550 74.7 10249 3 US-09-186-002-14  
25 550 74.7 10339 3 US-09-186-002-13  
26 548.4 74.5 10160 3 US-09-097-319A-8  
27 548.4 74.5 10160 3 US-09-097-319A-8  
28 548.4 74.5 11784 3 US-09-097-319A-9  
29 548.4 74.5 11784 3 US-09-097-319A-9  
30 548.4 74.5 11991 3 US-09-097-319A-10  
31 548.4 74.5 11991 3 US-09-097-319A-10  
32 548.4 74.5 11991 3 US-09-097-319A-10  
33 548.4 74.5 11991 3 US-09-097-319A-10  
34 534.6 72.6 5767 3 US-09-810-861B-4  
35 534.6 72.6 5767 3 US-09-810-861B-4  
36 526 71.5 12614 3 US-09-577-424-1  
37 514.4 69.9 10252 3 US-09-186-002-15  
38 505.6 68.7 5033 2 US-08-038-768A-1  
39 476.8 64.8 2728 3 US-08-036-402B-7  
40 459.2 62.4 1138 3 US-09-011-151-8  
41 459.2 62.4 1138 3 US-09-011-151-8  
42 459 62.4 1742 3 US-09-737-626A-30  
43 459 62.4 1742 3 US-09-737-626A-30  
44 459 62.4 1742 3 US-10-427-180-30  
45 459 62.4 1742 3 US-10-427-180-30

ALIGNMENTS

RESULT 1  
US-09-027-998A-33  
; Sequence 33, Application US/09027998A  
; Patent No. 6284949  
; GENERAL INFORMATION:  
; APPLICANT: Fischhoff, David A  
; INVENTOR: Fuchs, Roy L  
; TITLE OF INVENTION: Insect Resistant Plants  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold White and Durkee  
; STREET: PO Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM: disk  
; PROGRAM TYPE: FLOPPY disk  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,998A  
; FILING DATE: 23-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOST:195  
; TELEPHONE: 713-861-1490  
; INFORMATION FOR SEQ ID NO. 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 661 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-09-027-998A-33

Query Match 75.3%; Score 554; DB 3; Length 661;  
Best Local Similarity 94.5%; Pred. No. 1.4e-175;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;  
QY 116 TCTCGAGTCTTTCACGAGGCTATATCCGAACTCTCGATTCATTCG 175

Db 20 TCCGATGTGAGACTTTTCACAAAGGGTAAATATCCGGAAACCTCTCGGATTCGATGCC 79  
Oy 176 CAGCTATCTGTCACTTCATCAAAAGGACATGAAAGAGATGGCACTCAAAATGCC 235  
Db 80 CAGCTATCTGTCACTTCATGAAAGATGAAAGAGATGGCACTTCGAAATGCC 139  
Oy 236 ATCATTTGCGATTAAGAAAGGCTATGCTGCAAGATGCTGCGCAAGTGGTCCAAAG 235  
Db 140 ATCATTTGCGATTAAGAAAGGCTATGCTGCAAGATGCTGCGCAAGTGGTCCAAAG 199  
Oy 296 ATGGAACCCCAACCCAGAGAGCATGTGGAAAAAGAAAGAGTTCACACGCTTTCAA 355  
Db 200 ATGGAACCCCAACCCAGAGAGCATGTGGAAAAAGAAAGAGTTCACACGCTTTCAA 259  
Oy 356 AGCAATGGAATTAATGAT---TCAGTGAAGACTTTTCAAAAGGTAATTCGGA 411  
Db 260 AGCAATGGAATTAATGAT---TCAGTGAAGACTTTTCAAAAGGTAATTCGGA 319  
Oy 412 AACCTCTCGGATTCGATTCGCGCAATGCTGCACTTCGCAAAAGGTAATTCGGA 471  
Db 320 AACCTCTCGGATTCGATTCGCGCAATGCTGCACTTCGCAAAAGGTAATTCGGA 379  
Oy 472 GAAGTGGCACTTAAGATGCAATTCGCAATTAAGAAAGGCTATGCTTCAGATGCC 531  
Db 380 GAAGTGGCACTTAAGATGCAATTCGCAATTAAGAAAGGCTATGCTTCAGATGCC 439  
Oy 532 TCTGCGCAAGTGTGCTCCAAAGATGACCCCAACAGAGAGCATGCTGAAAGAA 591  
Db 440 TCTGCGCAAGTGTGCTCCAAAGATGACCCCAACAGAGAGCATGCTGAAAGAA 499  
Oy 592 GAGCTTCAACAGCTTTCAAAGAGTGAATGATATCTTCACATGAGTAAG 651  
Db 500 GAGCTTCAACAGCTTTCAAAGAGTGAATGATATCTTCACATGAGTAAG 559  
Oy 652 GATGAGCAACATCCCATCTTCCTGCAAGACCCCTCTCTATATAGAAAGTCAATT 711  
Db 560 GATGAGCAACATCCCATCTTCCTGCAAGACCCCTCTCTATATAGAAAGTCAATT 619  
Oy 712 CATTGAGAGAGACAGCTG 731  
Db 620 CATTGAGAGAGACAGCTG 639

RESULT 2  
US-09-943-692-33

Sequence 33, Application US/09943692  
Patent No. 6953835  
GENERAL INFORMATION:  
APPLICANT: FISCHHOFF, DAVID A.  
APPLICANT: FUCHS, ROY L.  
APPLICANT: MCHESON, STEVEN A.  
APPLICANT: MCHESON, STEVEN A.  
TITLE: COPIES OF THE DNA SEQUENCE OF THE BACILLUS THURINGIENSIS  
CURRENT APPLICATION NUMBER: US/09/943,692  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: 09/027,998  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: Patent version 3.1  
SEQ ID NO 33  
LENGTH: 661  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Recombinant Cauliflower Mosaic Viral Promoter (CAUVS5)  
US-09-943-692-33

Query Match 75.3%; Score 554; DB 3; Length 661;  
Best Local Similarity 94.5%; Pred. No. 1,4e-175;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Oy 116 TCTGATGTGAGACTTTTCACAAAGGTAATATCCGGAAACCTCTCGGATTCGATGCC 175  
Db 20 TCCGATGTGAGACTTTTCACAAAGGTAATATCCGGAAACCTCTCGGATTCGATGCC 79  
Oy 176 CAGCTATCTGTCACTTCATCAAAAGGACATGAAAGAGATGGCACTCAAAATGCC 235  
Db 80 CAGCTATCTGTCACTTCATGAAAGATGAAAGAGATGGCACTTCGAAATGCC 139  
Oy 236 ATCATTTGCGATTAAGAAAGGCTATGCTGCAAGATGCTGCGCAAGTGGTCCAAAG 295  
Db 140 ATCATTTGCGATTAAGAAAGGCTATGCTGCAAGATGCTGCGCAAGTGGTCCAAAG 199  
Oy 296 ATGGAACCCCAACCCAGAGAGCATGTGGAAAAAGAAAGAGTTCACACGCTTTCAA 355  
Db 200 ATGGAACCCCAACCCAGAGAGCATGTGGAAAAAGAAAGAGTTCACACGCTTTCAA 259  
Oy 356 AGCAATGGAATTAATGAT---TCAGTGAAGACTTTTCAAAAGGTAATTCGGA 411  
Db 260 AGCAATGGAATTAATGAT---TCAGTGAAGACTTTTCAAAAGGTAATTCGGA 319  
Oy 412 AACCTCTCGGATTCGATTCGCGCAATGCTGCACTTCGCAAAAGGTAATTCGGA 471  
Db 320 AACCTCTCGGATTCGATTCGCGCAATGCTGCACTTCGCAAAAGGTAATTCGGA 379  
Oy 472 GAAGTGGCACTTAAGATGCAATTCGCAATTAAGAAAGGCTATGCTTCAGATGCC 531  
Db 380 GAAGTGGCACTTAAGATGCAATTCGCAATTAAGAAAGGCTATGCTTCAGATGCC 439  
Oy 532 TCTGCGCAAGTGTGCTCCAAAGATGACCCCAACAGAGAGCATGCTGAAAGAA 591  
Db 440 TCTGCGCAAGTGTGCTCCAAAGATGACCCCAACAGAGAGCATGCTGAAAGAA 499  
Oy 592 GAGCTTCAACAGCTTTCAAAGAGTGAATGATATCTTCACATGAGTAAG 651  
Db 500 GAGCTTCAACAGCTTTCAAAGAGTGAATGATATCTTCACATGAGTAAG 559  
Oy 652 GATGAGCAACATCCCATCTTCCTGCAAGACCCCTCTCTATATAGAAAGTCAATT 711  
Db 560 GATGAGCAACATCCCATCTTCCTGCAAGACCCCTCTCTATATAGAAAGTCAATT 619  
Oy 712 CATTGAGAGAGACAGCTG 731  
Db 620 CATTGAGAGAGACAGCTG 639

RESULT 3  
US-09-441-340-29

Sequence 29, Application US/09441340  
Patent No. 6448476  
GENERAL INFORMATION:  
APPLICANT: BARRY, Gerard F.  
APPLICANT: BARRY, Gerard F.  
TITLE: COPIES OF THE DNA SEQUENCE OF THE BACILLUS THURINGIENSIS  
CURRENT APPLICATION NUMBER: US/09/441,340  
PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 60/108,763  
EARLIER FILING DATE: 1998-11-17  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patent ver. 2.0  
SEQ ID NO 29  
LENGTH: 2107  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette comprising plant operable promoter linked  
OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA  
OTHER INFORMATION: acetyltransferase, and termination sequence  
NAME/KEY: promoter  
LOCATION: (26)..(590)  
FEATURE:  
NAME/KEY: 5'UTR

LOCATION: (615)..(685)  
 FEATURE: intron  
 NAME/KEY: intron  
 LOCATION: (699)..(1148)  
 FEATURE: intron  
 NAME/KEY: intron  
 LOCATION: (1149)..(1426)  
 FEATURE: intron  
 NAME/KEY: intron  
 LOCATION: (1427)..(1858)  
 FEATURE: intron  
 NAME/KEY: intron  
 LOCATION: (1859)..(2102)  
 FEATURE: intron  
 NAME/KEY: intron  
 LOCATION: (2103)..(2107)  
 FEATURE: intron

Query Match  
 Seq. Local Similarity 75.3%; Score 554; DB 3; Length 2107;  
 Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;  
 QY 116 TCGCAGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 175  
 DB 28 TCGCAGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 87  
 QY 176 CAGCTATCTGTCACTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 235  
 DB 88 CAGCTATCTGTCACTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 147  
 QY 236 ATCATTCGATTAAGGAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 295  
 DB 148 ATCATTCGATTAAGGAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 207  
 QY 296 ATGACACCCCAACGAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 355  
 DB 208 ATGACACCCCAACGAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 267  
 QY 356 AGCAAGTGTGATGTGATGTATTTTCGAGTGTGAGCTTTTCAACAAAGGCTAATATGCC 411  
 DB 268 AGCAAGTGTGATGTGATGTATTTTCGAGTGTGAGCTTTTCAACAAAGGCTAATATGCC 327  
 QY 412 AACCTCTCGGATTCATATCGGGAACCTCTCGGATTCATATGCC 471  
 DB 328 AACCTCTCGGATTCATATCGGGAACCTCTCGGATTCATATGCC 387  
 QY 472 GAGGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 531  
 DB 388 GAGGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 447  
 QY 532 TCTGCCGACAGTGTGTCGGAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 591  
 DB 448 TCTGCCGACAGTGTGTCGGAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 507  
 QY 592 GAGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 651  
 DB 508 GAGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 567  
 QY 652 GATGACGACGATTCATATCGGGAACCTCTCGGATTCATATGCC 711  
 DB 568 GATGACGACGATTCATATCGGGAACCTCTCGGATTCATATGCC 627  
 QY 712 CATTTGGAGAGACACGCTG 731  
 DB 628 CATTTGGAGAGACACGCTG 647

RESULT 4  
 US-09-441-340-25  
 Sequence 25, Application US/09441340  
 Patent No. 6,446,000  
 GENERAL INFORMATION:  
 APPLICANT: Baxby, Gerard F.  
 TITLE OF INVENTION: Phosphonate Metabolizing Plants  
 FILE REFERENCE: 38-21(15303)  
 CURRENT APPLICATION NUMBER: US/09/441,340

CURRENT FILING DATE: 1999-11-15  
 EARLIER FILING DATE: 1998-11-17  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 25  
 LENGTH: 2122

ORGANISM: Artificial Sequence  
 OTHER INFORMATION: Description of Artificial Sequence expression  
 OTHER INFORMATION: cassette comprising plant promoter linked to  
 OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked  
 OTHER INFORMATION: to termination sequence

FEATURE:  
 NAME/KEY: promoter  
 LOCATION: (6)..(620)  
 FEATURE:  
 NAME/KEY: 5'UTR  
 LOCATION: (645)..(715)  
 NAME/KEY: intron  
 LOCATION: (729)..(1178)  
 FEATURE:  
 NAME/KEY: transit peptide  
 LOCATION: (1179)..(1406)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1407)..(1838)  
 FEATURE:  
 NAME/KEY: terminator  
 LOCATION: (1849)..(2082)

Query Match  
 Seq. Local Similarity 75.3%; Score 554; DB 3; Length 2122;  
 Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;  
 QY 116 TCGCAGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 175  
 DB 8 TCGCAGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 67  
 QY 176 CAGCTATCTGTCACTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 235  
 DB 68 CAGCTATCTGTCACTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 127  
 QY 236 ATCATTCGATTAAGGAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 295  
 DB 128 ATCATTCGATTAAGGAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 187  
 QY 296 ATGACACCCCAACGAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 355  
 DB 188 ATGACACCCCAACGAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 247  
 QY 356 AGCAAGTGTGATGTGATGTATTTTCGAGTGTGAGCTTTTCAACAAAGGCTAATATGCC 411  
 DB 248 AGCAAGTGTGATGTGATGTATTTTCGAGTGTGAGCTTTTCAACAAAGGCTAATATGCC 307  
 QY 412 AACCTCTCGGATTCATATCGGGAACCTCTCGGATTCATATGCC 471  
 DB 308 AACCTCTCGGATTCATATCGGGAACCTCTCGGATTCATATGCC 367  
 QY 472 GAGGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 531  
 DB 368 GAGGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 427  
 QY 532 TCTGCCGACAGTGTGTCGGAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 591  
 DB 428 TCTGCCGACAGTGTGTCGGAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 487  
 QY 592 GAGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 651  
 DB 498 GAGTGTGAGCTTTTCAACAAAGGCTAATATCGGGAACCTCTCGGATTCATATGCC 547

Oy 652 GATGACGACATCCCACTATCTTGGCAAGACCTTCTATATTAAGAGATTCAATT 711  
Db 548 GATGACGACATCCCACTATCTTGGCAAGACCTTCTATATTAAGAGATTCAATT 607  
Oy 712 CATTGGAGAGACACGCTG 731  
Db 608 CATTGGAGAGACACGCTG 627

## RESULT 5

US-09-441-340-31  
Sequence 31, Application US/09441340  
Patent No. 6448476  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard P.  
TITLE OF INVENTION: Phosphonate Metabolizing Plants  
FILE REFERENCE: 38-21(15303)  
CURRENT APPLICATION NUMBER: US/09/441,340  
PRIORITY DATE: 1998-11-17  
EARLIER APPLICATION NUMBER: 1,60,108,763  
BARLIER FILING DATE: 1998-11-17  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 31  
LENGTH: 2436  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: monocot  
OTHER INFORMATION: expression cassette comprising plant operable  
OTHER INFORMATION: linked to an infection, a sequence coding  
OTHER INFORMATION: for an AMP<sup>r</sup> acetyltransferase, and a termination  
OTHER INFORMATION: sequence  
FEATURE:  
NAME/KEY: Promoter  
LOCATION: (26)..(540)  
FEATURE:  
NAME/KEY: Intron  
LOCATION: (670)..(1473)  
FEATURE:  
NAME/KEY: transic peptide  
LOCATION: (1498)..(1725)  
NAME/KEY: CDS  
LOCATION: (1726)..(2157)  
FEATURE:  
NAME/KEY: terminator  
LOCATION: (2172)..(2427)

## US-09-441-340-31

Query Match 75.3%, Score 554, DB 3, Length 2436;  
Best Local Similarity 94.5%, Pctd. No. 2, 9e-175;  
Matches 586, Conservative 0, Mismatches 30, Indels 4, Gaps 1;

Oy 116 TCGGATGAGACTTTTCAACAAAGGTAAATCGGAAACCTCTCGGATTCGATGCC 175  
Db 28 TCGGATGAGACTTTTCAACAAAGGTAAATCGGAAACCTCTCGGATTCGATGCC 87  
Oy 176 CAGCTATCTGCACTTCATCAAAAGACAGTAAGAAAGAGAGGTGGCACTAAGGCC 235  
Db 88 CAGCTATCTGCACTTCATCTTATGTAAGTAAGTAAGAAAGAGGTGGCTCTAAGAGGCC 147  
Oy 236 ATCATTTGATTAAGAAAGGCTATGCTTCAAGATGCTCTCCGACAGTGTCCAAAG 295  
Db 148 ATCATTTGATTAAGAAAGGCTATGCTTCAAGATGCTCTCCGACAGTGTCCAAAG 207  
Oy 296 ATGAGACCCCAACAGAGAGCATCTGTGAAAGAAAGAAAGCTTCCACACAGCTTCAA 355  
Db 208 ATGAGACCCCAACAGAGAGCATCTGTGAAAGAAAGAAAGCTTCCACACAGCTTCAA 267  
Oy 356 ACGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411

Db 268 ACGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327  
Oy 412 AACCTCTGGATTCATTCGACAGCTATCTGTCACTTCAATCAAAAGACAGTAAGAAAG 471  
Db 338 AACCTCTGGATTCATTCGACAGCTATCTGTCACTTCAATCAAAAGACAGTAAGAAAG 387  
Oy 472 GAGGTGGACATTCAAATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 531  
Db 388 GAGGTGGACATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 447  
Oy 532 TCGGCAAGATGATTCGAAAG 591  
Db 448 TCGGCAAGATGATTCGAAAG 507  
Oy 592 GAGGTTCACACGCTTCAAGCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 651  
Db 508 GAGGTTCACACGCTTCAAGCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 567  
Oy 652 GATGACGACATCCCACTATCTTGGCAAGACCTTCTATATTAAGAGATTCAATT 711  
Db 568 GATGACGACATCCCACTATCTTGGCAAGACCTTCTATATTAAGAGATTCAATT 627  
Oy 712 CATTGGAGAGACACGCTG 731  
Db 628 CATTGGAGAGACACGCTG 647

## RESULT 6

US-09-377-4668-23  
Sequence 23, Application US/093774668  
Patent No. 6448476  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Ab Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Ab Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/09/377,4668  
PRIORITY DATE: 1999-08-19  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23  
LENGTH: 3469  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette  
NAME/KEY: Promoter  
LOCATION: (25)..(640)  
OTHER INFORMATION: P-CaMV.35S  
NAME/KEY: 5'UTR  
LOCATION: (664)..(734)  
OTHER INFORMATION: L-Ta.hcb1  
NAME/KEY: Intron  
LOCATION: (748)..(1238)  
OTHER INFORMATION: I-Ob.Acl1  
NAME/KEY: CDS  
LOCATION: (1241)..(3199)  
OTHER INFORMATION: Cry3Bb1 variant 11231mv2  
NAME/KEY: terminator  
LOCATION: (3217)..(3450)  
OTHER INFORMATION: T-Ta.hsp17

## US-09-377-4668-23

Query Match 75.3%, Score 554, DB 3, Length 3469;  
Best Local Similarity 94.5%, Pctd. No. 3, 5e-175;  
Matches 586, Conservative 0, Mismatches 30, Indels 4, Gaps 1;

Oy 116 TCGGATGAGACTTTTCAACAAAGGTAAATCGGAAACCTCTCGGATTCGATGCC 175  
Db 28 TCGGATGAGACTTTTCAACAAAGGTAAATCGGAAACCTCTCGGATTCGATGCC 87  
Oy 176 CAGCTATCTGCACTTCATCAAAAGACAGTAAGAAAGAGAGGTGGCACTAAGGCC 235

```
Db 88 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAGGAGGTGGCTCTTCAAAATGCC 147
Qy 236 ATCAATTCGGATTAAGGAAAGGCTATCTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 295
Db 148 ATCAATTCGGATTAAGGAAAGGCTATCTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 207
Qy 296 ATGACACCCCAACCCACGAGGAGCATGCTGGAAAGGAGAGCTTCCCAACAGCTCTCA 355
Db 208 ATGACACCCCAACCCACGAGGAGCATGCTGGAAAGGAGAGCTTCCCAACAGCTCTCA 267
Qy 356 AGCAATGTGATGTGATGAT-----TGCAGTGAAGCTTTTCAACAAAGGCTATATATCGGA 411
Db 268 AGCAATGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327
Qy 412 AACCTCTCGGATTCATTTGCCGAGTATCTGTCATCTTCAAAAGGAGCATGAGAAAG 471
Db 328 AACCTCTCGGATTCATTTGCCGAGTATCTGTCATCTTCAAAAGGAGCATGAGAAAG 387
Qy 472 GAGGTGGACCTCAAAATGCCATCTTGGATTAAGGAGAGGCTATGCTTCAAGATGCC 531
Db 388 GAGGTGGCTCTCTACAAATGCCATCTTGGATTAAGGAGAGGCTATGCTTCAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACGAGGAGCATCTGGGAAAGGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACGAGGAGCATCTGGGAAAGGAA 507
Qy 592 GAGCTTCCAAACAAGCTCTTCAAAAGCAAGTGGATGTGATGTGATGTGATGTGATGTGAT 651
Db 508 GAGCTTCCAAACAAGCTCTTCAAAAGCAAGTGGATGTGATGTGATGTGATGTGATGTGAT 567
Qy 652 GATGACGACATCCCATCTTCTTCCGAGAGCTCTCTCTATATAGGAGTTCATTT 711
Db 568 GATGACGACATCCCATCTTCTTCCGAGAGCTCTCTCTATATAGGAGTTCATTT 627
Qy 712 CATTTGGAGAGGACAGCTG 731
Db 628 CATTTGGAGAGGACAGCTG 647
```

## RESULT 7

US-10-232-665-23 Application US/10232665

Sequence 23 (6498)

Patent No. 6501009

GENERAL INFORMATION:

APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/10/232,665

CURRENT FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US/09/377,466

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 23

LENGTH: 3469

TYPE: DNA

ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: expression

FEATURE:

NAME/KEY: promoter

LOCATION: (25)..(640)

OTHER INFORMATION: P-CMV.355

FEATURE:

NAME/KEY: 5'UTR

LOCATION: (664)..(734)

OTHER INFORMATION: L-Ta.hcbl

FEATURE:

NAME/KEY: intron

LOCATION: (748)..(1238)

OTHER INFORMATION: I-Ob.Act1

FEATURE:

NAME/KEY: 3'UTR

LOCATION: (1248)..(1318)

OTHER INFORMATION: L-Ta.hcbl

FEATURE:

NAME/KEY: polyA

LOCATION: (1328)..(1398)

OTHER INFORMATION: L-Ta.hcbl

FEATURE:

NAME/KEY: 3'UTR

LOCATION: (1408)..(1478)

OTHER INFORMATION: L-Ta.hcbl

FEATURE:

NAME/KEY: polyA

LOCATION: (1488)..(1558)

OTHER INFORMATION: L-Ta.hcbl

FEATURE:

NAME/KEY: 3'UTR

LOCATION: (1568)..(1638)

OTHER INFORMATION: L-Ta.hcbl

FEATURE:

NAME/KEY: polyA

LOCATION: (1648)..(1718)

OTHER INFORMATION: L-Ta.hcbl

FEATURE:

NAME/KEY: 3'UTR

LOCATION: (1728)..(1798)

OTHER INFORMATION: L-Ta.hcbl

FEATURE:

NAME/KEY: polyA

LOCATION: (1808)..(1878)

OTHER INFORMATION: L-Ta.hcbl

NAME/KEY: CDS  
LOCATION: (1241)..(3199)  
OTHER INFORMATION: Cry3Bb1 variant 11231mv2  
FEATURE:  
NAME/KEY: terminator  
LOCATION: (3217)..(3450)  
OTHER INFORMATION: T-Ta.hcp17  
US-10-232-665-23

Query Match 75.3%; Score 554; DB 3; Length 3469;  
Best Local Similarity 94.5%; Read N; 3, 2, 175;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCAGTGAAGCTTTTCAACAAAGGCTATATCGGGAACCTCTCTCGATTCATTCATGCC 175  
Db 28 TCCGATGTGAGACTTTTCAACAAAGGCTATATCGGGAACCTCTCTCGATTCATTCATGCC 87  
Qy 176 CAGCTATCTGTCACTTTTCAACAAAGGCTATATCGGGAACCTCTCTCGATTCATTCATGCC 235  
Db 88 CAGCTATCTGTCACTTTTCAACAAAGGCTATATCGGGAACCTCTCTCGATTCATTCATGCC 147  
Qy 236 ATCAATTCGGATTAAGGAAAGGCTATCTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 295  
Db 148 ATCAATTCGGATTAAGGAAAGGCTATCTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 207  
Qy 296 ATGACACCCCAACCCACGAGGAGCATGCTGGAAAGGAGAGCTTCCCAACAGCTCTCA 355  
Db 208 ATGACACCCCAACCCACGAGGAGCATGCTGGAAAGGAGAGCTTCCCAACAGCTCTCA 267  
Qy 356 AGCAATGTGATGTGATGAT-----TGCAGTGAAGCTTTTCAACAAAGGCTATATATCGGA 411  
Db 268 AGCAATGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327  
Qy 412 AACCTCTCGGATTCATTTGCCGAGTATCTGTCATCTTCAAAAGGAGCATGAGAAAG 471  
Db 328 AACCTCTCGGATTCATTTGCCGAGTATCTGTCATCTTCAAAAGGAGCATGAGAAAG 387  
Qy 472 GAGGTGGACCTCAAAATGCCATCTTGGATTAAGGAGAGGCTATGCTTCAAGATGCC 531  
Db 388 GAGGTGGCTCTCTACAAATGCCATCTTGGATTAAGGAGAGGCTATGCTTCAAGATGCC 447  
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACGAGGAGCATCTGGGAAAGGAA 591  
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACGAGGAGCATCTGGGAAAGGAA 507  
Qy 592 GAGCTTCCAAACAAGCTCTTCAAAAGCAAGTGGATGTGATGTGATGTGATGTGATGTGAT 651  
Db 508 GAGCTTCCAAACAAGCTCTTCAAAAGCAAGTGGATGTGATGTGATGTGATGTGATGTGAT 567  
Qy 652 GATGACGACATCCCATCTTCTTCCGAGAGCTCTCTCTATATAGGAGTTCATTT 711  
Db 568 GATGACGACATCCCATCTTCTTCCGAGAGCTCTCTCTATATAGGAGTTCATTT 627  
Qy 712 CATTTGGAGAGGACAGCTG 731  
Db 628 CATTTGGAGAGGACAGCTG 647

## RESULT 8

US-09-377-466B-15

Sequence 15; Application US/09377466B

Patent No. 6501009

GENERAL INFORMATION:

APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/09/377,466B

CURRENT FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 15

LENGTH: 1954

TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
NAME/KEY: Promoter  
LOCATION: (25)..(640)  
OTHER INFORMATION: P-CMV.35S  
NAME/KEY: Intron  
LOCATION: (669)..(1472)  
OTHER INFORMATION: I-Zm.Hsp70  
NAME/KEY: CDS  
LOCATION: (1490)..(3448)  
OTHER INFORMATION: Cry3Bb1 variant v11231  
NAME/KEY: terminator  
LOCATION: (3475)..(3730)  
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription  
OTHER INFORMATION: termination and polyadenylation sequence  
US-03-377-466-15

Query Match 75.3%; Score 554; DB 3; Length 3754;  
Best Local Similarity 94.5%; Pred. No. 3.6e-175;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

116 TCTGACGAGAGACCTTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 175  
28 TCCGATGTGAGACCTTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 87  
176 CAGCTATCTGCTCACTTCATCAAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 235  
88 CAGCTATCTGCTCACTTCATCAAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 147  
236 ATCATGTGAGATTAAGAAAGGATATATCGGAAACCTCTCGGATTCGATTCGATTCG 295  
148 ATCATGTGAGATTAAGAAAGGATATATCGGAAACCTCTCGGATTCGATTCGATTCG 207  
296 ATGACACCCACCCACGAGGACATGTGTGAAAGAAAGGATTCGATTCGATTCGATTCG 355  
208 ATGACACCCACCCACGAGGACATGTGTGAAAGAAAGGATTCGATTCGATTCGATTCG 267  
356 AGCAAGTGAATGATGTAT---TGCAGTGAACCTTTTCAAAAGGATATATCGGAA 411  
268 AGCAAGTGAATGATGTAT---TGCAGTGAACCTTTTCAAAAGGATATATCGGAA 327  
412 AACCTCTGAGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 471  
328 AACCTCTGAGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 387  
472 GAAGGTGAGACCTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCGATTCG 531  
388 GAAGGTGAGACCTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCGATTCG 447  
532 TCTGACGAGAGACCTTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 591  
448 TCTGACGAGAGACCTTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 507  
592 GACGTTCACACGCTTCCTCAAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 651  
508 GACGTTCACACGCTTCCTCAAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 567  
652 GATGACGACCAATCCGATTCCTTCGCAAGCCCTCTCTCATATTAAGAAAGTTCATTT 711  
568 GATGACGACCAATCCGATTCCTTCGCAAGCCCTCTCTCATATTAAGAAAGTTCATTT 627  
712 CATTTGAGAGACACGCTG 731  
628 CATTTGAGAGACACGCTG 647

RESULT 9  
US-10-232-665-15  
Sequence 15; Application US/10232665  
Patent No. 6943281  
GENERAL INFORMATION:

APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/10/232,665  
PRIORITY DATE: 05/10/2002  
PRIORITY NUMBER: US/02/377,466  
PRIORITY DATE: 1998-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 15  
LENGTH: 3754  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
NAME/KEY: Promoter  
LOCATION: (25)..(640)  
OTHER INFORMATION: P-CMV.35S  
NAME/KEY: Intron  
LOCATION: (669)..(1472)  
OTHER INFORMATION: I-Zm.Hsp70  
NAME/KEY: CDS  
LOCATION: (1490)..(3448)  
OTHER INFORMATION: Cry3Bb1 variant v11231  
NAME/KEY: terminator  
LOCATION: (3475)..(3730)  
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription  
OTHER INFORMATION: termination and polyadenylation sequence  
US-10-232-665-15

Query Match 75.3%; Score 554; DB 3; Length 3754;  
Best Local Similarity 94.5%; Pred. No. 3.6e-175;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

116 TCTGACGAGAGACCTTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 175  
28 TCCGATGTGAGACCTTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 87  
176 CAGCTATCTGCTCACTTCATCAAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 235  
88 CAGCTATCTGCTCACTTCATCAAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 147  
236 ATCATGTGAGATTAAGAAAGGATATATCGGAAACCTCTCGGATTCGATTCGATTCG 295  
148 ATCATGTGAGATTAAGAAAGGATATATCGGAAACCTCTCGGATTCGATTCGATTCG 207  
296 ATGACACCCACCCACGAGGACATGTGTGAAAGAAAGGATTCGATTCGATTCGATTCG 355  
208 ATGACACCCACCCACGAGGACATGTGTGAAAGAAAGGATTCGATTCGATTCGATTCG 267  
356 AGCAAGTGAATGATGTAT---TGCAGTGAACCTTTTCAAAAGGATATATCGGAA 411  
268 AGCAAGTGAATGATGTAT---TGCAGTGAACCTTTTCAAAAGGATATATCGGAA 327  
412 AACCTCTGAGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 471  
328 AACCTCTGAGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 387  
472 GACGTTCACACGCTTCCTCAAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 531  
388 GACGTTCACACGCTTCCTCAAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 447  
532 TCTGACGAGAGACCTTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 591  
448 TCTGACGAGAGACCTTTCACAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 507  
592 GACGTTCACACGCTTCCTCAAAAGGATATATCGGAAACCTCTCGGATTCGATTCG 651

Db 508 GACGTTCCCAACACGCTCTTCAAAGCAAGTGGATTGATGATATCTTCACTGAGTAAGG 567  
Qy 652 GATGACGCAAAATCCCACTATCTTCCGAGACCCCTTCTCTATATATAAGGAAGTTCATTT 711  
Db 568 GATGACGCAAAATCCCACTATCTTCCGAGACCCCTTCTCTATATATAAGGAAGTTCATTT 627  
Qy 712 GATTTCGAGAGAGAGAGCTG 731  
Db 628 CATTTCGAGAGAGAGAGCTG 647

## RESULT 10

US-09-182-117-1

; Sequence 1, Application US/09182117

; Patent No. 6204436

; GENERAL INFORMATION:

; APPLICANT: MANNERLOEF, Marie

; TITLE OF INVENTION: Transgenic Plant

; NUMBER OF SEQUENCES: 2

; COMPUTER READABLE FORM: 2

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/182.117

; FILING DATE:

; CLASSIFICATION:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8012 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-09-182-117-1

Query Match 75.3%; Score 554; DB 3; Length 8012;

Best Local Similarity 94.5%; Pred. No. 5.4e-175;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGAGTGGAGCTTTTCAACAAAGGGTAAATATCGGAAACCTCTCTCGGATTTCATTTGCC 175  
Db 3044 TCGGATGGAGCTTTTCAACAAAGGGTAAATATCGGAAACCTCTCTCGGATTTCATTTGCC 3103  
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAGGAGGTGGCAGCTACCAATGCC 235  
Db 3104 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAGGAGGTGGCCTCTCAAAATGCC 3163

Qy 236 ATCAATTGGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGAGTGCTCCCAAG 295  
Db 3164 ATCAATTGGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGAGTGCTCCCAAG 3223  
Qy 296 ATGGAACCCCAACCCACGAGGAGCATCGTGGAAAAAGAGACGTTTCAACCAAGCTTTCAA 355  
Db 3224 ATGGAACCCCAACCCACGAGGAGCATCGTGGAAAAAGAGACGTTTCAACCAAGCTTTCAA 3283

Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGGAGCTTTTCAACAAAGGGTAAATATCGGGA 411  
Db 3284 AGCAAGTGGATTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 3343  
Qy 412 AACCTCTCTCGGATTTCATTTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGG 471  
Db 3344 AACCTCTCTCGGATTTCATTTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGG 3403

Qy 472 GAAGGTGGCACTTCAAAATGCCATCATTTGGGATAAAGGAAAGGCTATCGTTCAAGATGCC 531  
Db 3404 GAAGGTGGCTCTTCAAAATGCCATCATTTGGGATAAAGGAAAGGCTATCGTTCAAGATGCC 3463  
Qy 532 TCTGCGGACAGTGGTCCAAAGATGAGACCCCAACCCACGAGGAGCATCTGCGAAAAAGAA 591

Db 3464 TCTGCGGACAGTGGTCCAAAGATGAGACCCCAACCCACGAGGAGCATCTGCGAAAAAGAA 3523  
Qy 592 GAGGTTTCAACCAAGCTTTTCAAGCAAGTGAATGATGTGATATCTTCACTGAGCTAAGG 651  
Db 3524 GAGGTTTCAACCAAGCTTTTCAAGCAAGTGAATGATGTGATATCTTCACTGAGCTAAGG 3583  
Qy 652 GATGACGCAAAATCCCACTATCTTCCGAGACCCCTTCTCTATATATAAGGAAGTTCATTT 711  
Db 3584 GATGACGCAAAATCCCACTATCTTCCGAGACCCCTTCTCTATATATAAGGAAGTTCATTT 3643  
Qy 712 CATTTCGAGAGAGAGAGCTG 731  
Db 3644 CATTTCGAGAGAGAGAGCTG 3663

## RESULT 11

US-09-434-039A-1

; Sequence 1, Application US/09434039A

; Patent No. 6531649

; GENERAL INFORMATION:

; APPLICANT: MANNERLOEF, Marie

; TITLE OF INVENTION: Transgenic Plant

; NUMBER OF SEQUENCES: 2

; COMPUTER READABLE FORM: 2

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/434.039A

; FILING DATE:

; CLASSIFICATION:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8012

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-09-434-039A-1

Query Match 75.3%; Score 554; DB 3; Length 8012;

Best Local Similarity 94.5%; Pred. No. 5.4e-175;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGAGTGGAGCTTTTCAACAAAGGGTAAATATCGGAAACCTCTCTCGGATTTCATTTGCC 175  
Db 3044 TCGGATGGAGCTTTTCAACAAAGGGTAAATATCGGAAACCTCTCTCGGATTTCATTTGCC 3103  
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAGGAGGTGGCAGCTACCAATGCC 235  
Db 3104 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAGGAGGTGGCTCTCAAAATGCC 3163

Qy 236 ATCAATTGGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGAGTGCTCCCAAG 295  
Db 3164 ATCAATTGGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGAGTGCTCCCAAG 3223  
Qy 296 ATGGAACCCCAACCCACGAGGAGCATCGTGGAAAAAGAGACGTTTCAACCAAGCTTTCAA 355  
Db 3224 ATGGAACCCCAACCCACGAGGAGCATCGTGGAAAAAGAGACGTTTCAACCAAGCTTTCAA 3283

Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGGAGCTTTTCAACAAAGGGTAAATATCGGGA 411  
Db 3284 AGCAAGTGGATTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 3343  
Qy 412 AACCTCTCTCGGATTTCATTTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGG 471  
Db 3344 AACCTCTCTCGGATTTCATTTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGG 3403

Qy 472 GAAGGTGGCACTTCAAAATGCCATCATTTGGGATAAAGGAAAGGCTATCGTTCAAGATGCC 531  
Db 3404 GAAGGTGGCTCTTCAAAATGCCATCATTTGGGATAAAGGAAAGGCTATCGTTCAAGATGCC 3463  
Qy 532 TCTGCGGACAGTGGTCCAAAGATGAGACCCCAACCCACGAGGAGCATCTGCGAAAAAGAA 591

**Tue Jun 6 08:26:39 2006**

us-10-075-105c-1.rn1

**Page 8**

Db	3464	TCGTCCACACAGTGGTCCCAAGATGGAACCCCAACCAAGAGATGCTGGAAAAAGAA	3523
Qy	592	GAGCTTCCACACAGCTCTTCAAGAGAGTGAATTGATATGTCATCAAGACGTAAG	651
Db	3524	GAGCTTCCACACAGCTCTTCAAGAGAGTGAATTGATATGTCATCAAGACGTAAG	3583
Qy	652	GATGACCAACATCCCATCTATCTCTGGCAAGACCTCTCTATATAAGAAAGTGAATT	711
Db	3584	GATGACCAACATCCCATCTATCTCTGGCAAGACCTCTCTATATAAGAAAGTGAATT	3643
Qy	712	CATTTGAGAGGAGACAGCTG	731
Db	3644	CATTTGAGAGGAGACAGCTG	3663

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US-09-186-002-16
RESULT 12
Sequence ID: 16 Application US/09186002B
Sequence ID: 16 Application US/09186002B
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
TITLE OF INVENTION: Improved Method for Transforming Plants to Express
TITLE OF INVENTION: delta Endotoxins
CURRENT PRIORITY: 09/110547 US Pat. No. 6489542 09/186,002
CURRENT FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 8349
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: gene (3666) ..(5573)
OTHER INFORMATION: completely synthesized
US-09-186-002-16

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Query Match 75.3%; Score 554; DB 3; Length 8349;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1

Oy 116 TCGCAGTGAAGACCTTTTCACAAAGGTAATTCGGAAACCTTCGATATTCACATGCG 175  
 Db 1807 TCCGATGTGAGACTTTTCACAAAGGTAATTCGGAAACCTTCGATATTCACATGCG 1866  
 Oy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTGAAGAAAGGAGTGGCCACTCAAAATGCG 235  
 Db 1867 CAGCTATCTGTCACTTATGTGTGAATATGTAAAGAAAGGATGGCTCTCTCAAAATGCG 235  
 Oy 236 ATCATTTGCTATTAAGAAAGGCTATTCGTCAAGATGGCTTCGCCACAGTGGTCTCCAAAG 1925  
 Db 1927 ATTCATTTGCTATTAAGAAAGGCTATTCGTCAAGATGGCTTCGCCACAGTGGTCTCCAAAG 1986  
 Oy 296 ATGGAACCCCAACCAAGAGCGCTGTGGAAAGAAAGAAAGCAAGCAAGTCTTCA 355  
 Db 1987 ATGGAACCCCAACCAAGAGCGCTGTGGAAAGAAAGAAAGCAAGTCTTCA 2046  
 Oy 356 AGCAATGGAATGGAATGTGAT----TGCAGTGAAGACTTTTCACAAAGGTAATTCGGGA 411  
 Db 2047 AGCAATGGAATGGAATGTGATGTGATGCAGATGTGAAGACTTTTCACAAAGGTAATTCGGGA 2106  
 Oy 412 AACCTCTCGAATTCACAGGCCCGACGCTATCTGTCACTTCATCAAAAGACAGTGAAGAG 471  
 Db 2107 AACCTCTCGAATTCACAGGCCCGACGCTATCTGTCACTTCATTCGAATGAGTGAAGAG 2166  
 Oy 472 GAAGGTGCACTTCGAATTCGATTCGGAATTAAGAAAGAGGCTATTCGTTCAGATGCG 531  
 Db 2167 GAAGGTGCTCTTCGAATTCGATTCGGAATTAAGAAAGAGGCTATTCGTTCAGATGCG 2222  
 Oy 532 TCGGCGCAAGTGTGCTCCAAAGATGGAACCCCAACCAAGAGCAAGTGTGTGAAAAAGAA 591

Db	2237	TCGCGCAAGATGGTGTCCCAAGAGGACCCCGACGAGAGGATCTGTGGAAAAAATA	2238
Qy	592	GACGTTCCAAACCAAGTCTCAAGAGAGTGATATTAATCTCACTGACGTAAAG	651
Db	2287	GAGGTGCGCAACCAAGTCTCAAGAGAGTGATATTAATCTCACTGACGTAAAG	2346
Qy	652	GAGGTGCGCAACCAAGTCTCTGTGGCAAGCCCTCTCTAATATPAGGAAGTCAATT	711
Db	2347	GATGACCCCAATCTCCATCTCTGTGGCAAGCCCTCTCTAATATPAGGAAGTCAATT	2406
Qy	712	CATTGGAGAGAGAAAGCTGT	731
Db	2407	CATTGGAGAGAGAAAGCTGT	2426

1 RESULT 13  
 2 US-09-182-117-5  
 3 Sequence 5, Application US/09182117  
 4 Filing Date: 09/18/2009  
 5 GENERAL INFORMATION:  
 6 APPLICANT:  
 7 TITLE OF INVENTION: Transgenic Plant  
 8 NUMBER OF SEQUENCES: 27  
 9 COMPUTER READABLE FORM:  
 10 MEDIA TYPE: Floppy disk  
 11 COMPUTER: IBM PC compatible  
 12 SOFTWARE: SYBASE, GENSTAT, DOS  
 13 CURRENT APPLICATION DATA:  
 14 APPLICATION NUMBER: US/09/182,117  
 15 FILING DATE:  
 16 CLASSIFICATION:  
 17 INFORMATION FOR SEQ ID NO: 5:  
 18 SEQUENCE CHARACTERISTICS:  
 19 LENGTH: 8000  
 20 TYPE: nucleic acid  
 21 STRANDEDNESS: double  
 22 TOPOLOGY: linear  
 23 MOLECULE TYPE: DNA (genomic)  
 24 HYPOTHETICAL: NO  
 25 ANTI-SENSE: NO  
 26 US-09-182-117-5

Query Match	75.3%	Score 554	DB 3	Length 8418
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Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1.

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Oy      1116  TCGAGATGAGACTTTTCAACAAAGGGTATATGGGAAACCTCTCGATTCATATGCG      175
Db      3023  TCGAGATGAGACTTTTCAACAAAGGGTATATCGGAAACCTCTCGATTCATATGCG      3089
Oy      176  CAGCTATCTGTCACTTCAACAAAGCAGTGAAGAAAGAGGTGCACTTCAAAATGCG      215
Db      3089  CAGCTATCTGTCACTTATATGTAAGAAATAGTGAAGAAAGGTGCACTTCAAAATGCG      3145
Oy      236  ATCATATGCTGTAAAGAGATACCTTCAAGATGCTGCGACAGAGGTGTCCTCAAG      285
Db      3143  ATCATATGCTGTAAAGAAAGGCATCGTTGAAGATGCTCTGCGACAGAGGTCTCAAG      3202
Oy      296  ATGAGACCCCAACCAAGAGAGATCGTGGAAAAAGAGAGGTTCACCAACGCTTTCA      355
Db      3203  ATGAGACCCCAACCAAGAGAGATCGTGGAAAAAGAGAGGTTCACCAACGCTTTCA      3262
Oy      356  AGCAAGTGAATTAATGTAT---TGCAGTGAACCTTTCAACAAAGGTAAATATGGGA      411
Db      3263  AGCAAGTGAATTAATGATATGTCGATATGAGACTTTCAACAAAGGTAAATATGGGA      3322
Oy      412  AACCTCCCTGGAGATTCATATGCGACAGATATCTGTCACTCAACAAAGCAATGAAAG      471
Db      3323  AACCTCCCTGGAGATTCATATGCGACACTATCTGTCACTTATATGTAAGATATGCGAAAG      3389
Oy      472  GAAGGTGGACCTCAAAATGCAATATTTGGATTAAGAAAGAGGCTATCGTCAAGATGCG      531

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Db 3383 GAAGGTGGCTCTCAAAATGCCATTCATTCGGATTAAGGAAGGCCATCGTTGAAGATGCC 3442  
Qy 532 TCTGCCGACAGAGTGTCCCAAAGATGAGACCCCAACGAGAGAGCATCGTGGAAAAGAA 591  
Db 3443 TCTGCCGACAGAGTGTCCCAAAGATGAGACCCCAACGAGAGAGCATCGTGGAAAAGAA 3502  
Qy 592 GAGCTTCCACACAGCTCTTCAAGACAGTGGATGTGATGTATCTCCACTGAGTAAGG 651  
Db 3503 GAGCTTCCACACAGCTCTTCAAGACAGTGGATGTGATGTATCTCCACTGAGTAAGG 3562  
Qy 652 GATGAGGACATCCCACTATCTTCGCAAGCCCTTCTCTATATAGGAAGTTCATTT 711  
Db 3563 GATGAGGACATCCCACTATCTTCGCAAGCCCTTCTCTATATAGGAAGTTCATTT 3622  
Qy 712 CATTTGGAGAGACAGCGCTG 731  
Db 3623 CATTTGGAGAGACAGCGCTG 3642

RESULT 14  
US-09-434-039A-5  
Query Match  
Best Local Similarity 75.3%; Score 554; DB 3; Length 8418;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;  
US-09-434-039A-5  
Sequence 5 Application US/09434039A  
Patent No. 6531649  
GENERAL INFORMATION:  
APPLICANT: WANNERLOEF, Marie  
APPLICANT: TENNING, Paul Peter  
APPLICANT: STEEN, Per  
TITLE OF INVENTION: Transgenic Plants  
FILE REFERENCE: 09/434,039  
CURRENT APPLICATION NUMBER: US/09/434,039A  
CURRENT FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/112,003  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 09/182,117  
PRIOR FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: patentin version 3.0  
SEQ ID NO 5  
LENGTH: 8418  
TYPE: DNA  
ORGANISM: Sugar beet

Qy 116 TCTGCAGTGAGACTTTTCAACAAGGGTAAATATCGGAAACCTCTCGGATTCATTCGCC 175  
Db 3023 TCCGATGTGAGACTTTTCAACAAGGGTAAATATCGGAAACCTCTCGGATTCATTCGCC 3082  
Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAGGTGGACCTACAAATGCC 235  
Db 3083 CAGCTATCTGTCACTTTATGTGAAGATAGTGGAAAAGGAGGTGGCTCTCTACAAATGCC 3142  
Qy 236 ATCATTCGATTAAGGAAGGCTATCGTTCAGAGAGTGGTTCGCAAGGTGTCCTCAAG 295  
Db 3143 ATCATTCGATTAAGGAAGGCTATCGTTCAGAGAGTGGTTCGCAAGGTGTCCTCAAG 3202  
Qy 296 ATGAGACCCCAACGAGGAGCATCGTTCGAAAAGGAGGTTCGCAAGGTGTCCTCAAG 355  
Db 3203 ATGAGACCCCAACGAGGAGCATCGTTCGAAAAGGAGGTTCGCAAGGTGTCCTCAAG 3262  
Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAGGGTAAATATCGGGA 411  
Db 3263 AGCAAGTGGATTGATGTGATGGTTCGAGTGTGAGACTTTTCAACAAGGGTAAATATCGGGA 3322  
Qy 412 AACCTCTCGGATTCGATTCGCAAGGTATCTGTCACTTCATCAAAAGGACAGTAGAAGG 471  
Db 3323 AACCTCTCGGATTCGATTCGCAAGGTATCTGTCACTTCATCAAAAGGACAGTAGAAGG 3382  
Qy 472 GAAGCTGCGACCTACAAATGCCATTCATTCGGATTAAGGAAGGCCATCGTTGAAGATGCC 531

Db 3383 GAAGGTGGCTCTCAAAATGCCATTCATTCGGATTAAGGAAGGCCATCGTTGAAGATGCC 3442  
Qy 532 TCTGCCGACAGAGTGTCCCAAAGATGAGACCCCAACGAGAGAGCATCGTGGAAAAGAA 591  
Db 3443 TCTGCCGACAGAGTGTCCCAAAGATGAGACCCCAACGAGAGAGCATCGTGGAAAAGAA 3502  
Qy 592 GAGCTTCCACACAGCTCTTCAAGACAGTGGATGTGATGTATCTCCACTGAGTAAGG 651  
Db 3503 GAGCTTCCACACAGCTCTTCAAGACAGTGGATGTGATGTATCTCCACTGAGTAAGG 3562  
Qy 652 GATGAGGACATCCCACTATCTTCGCAAGCCCTTCTCTATATAGGAAGTTCATTT 711  
Db 3563 GATGAGGACATCCCACTATCTTCGCAAGCCCTTCTCTATATAGGAAGTTCATTT 3622  
Qy 712 CATTTGGAGAGACAGCGCTG 731  
Db 3623 CATTTGGAGAGACAGCGCTG 3642

RESULT 15  
US-09-182-117-4  
Query Match  
Best Local Similarity 75.3%; Score 554; DB 3; Length 8798;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;  
US-09-182-117-4  
Sequence 4 Application US/09182117  
Patent No. 6294316  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Transgenic Plant  
NUMBER OF SEQUENCES: 27  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA: US/09/182,117  
PRIOR APPLICATION NUMBER: 09/182,117  
PRIOR FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 4  
CLASSIFICATION:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8798 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

Qy 116 TCTGCAGTGAGACTTTTCAACAAGGGTAAATATCGGAAACCTCTCGGATTCATTCGCC 175  
Db 3133 TCCGATGTGAGACTTTTCAACAAGGGTAAATATCGGAAACCTCTCGGATTCATTCGCC 3192  
Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAGGTGGACCTACAAATGCC 235  
Db 3193 CAGCTATCTGTCACTTTATGTGAAGATAGTGGAAAAGGAGGTGGCTCTCTACAAATGCC 3252  
Qy 236 ATCATTCGATTAAGGAAGGCTATCGTTCAGAGAGTGGTTCGCAAGGTGTCCTCAAG 295  
Db 3253 ATCATTCGATTAAGGAAGGCTATCGTTCAGAGAGTGGTTCGCAAGGTGTCCTCAAG 3312  
Qy 296 ATGAGACCCCAACGAGGAGCATCGTTCGAAAAGGAGGTTCGCAAGGTGTCCTCAAG 355  
Db 3313 ATGAGACCCCAACGAGGAGCATCGTTCGAAAAGGAGGTTCGCAAGGTGTCCTCAAG 3372  
Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAGGGTAAATATCGGGA 411  
Db 3373 AGCAAGTGGATTGATGTGATGGTTCGAGTGTGAGACTTTTCAACAAGGGTAAATATCGGGA 3432  
Qy 412 AACCTCTCGGATTCGATTCGCAAGGTATCTGTCACTTCATCAAAAGGACAGTAGAAGG 471

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Db      3433 AACCTCTCGAATTCATTCGCCAGCTATCTGTCACTTATTGTGAAAGATGGAAG 3492
Oy      472  GANAGTGGCACTTAAATGSCATTCATTCGATTAAGAAAGCTATGTTCAAGATGCC 531
Db      3493 GANAGTGGCTCTTAAATGSCATTCATTCGATTAAGAAAGCTATGTTCAAGATGCC 3552
Oy      532  TCTGCCGACAGTGTCTCCAAAGATGAACTCCCACTCAAGAGAGCATCTGAAAAAGAA 591
Db      3553 TCTGCCGACAGTGTCTCCAAAGATGAACTCCCACTCAAGAGAGCATCTGAAAAAGAA 3612
Oy      592  GAGGTTCCAAACGAGTGTCCAAAGATGAACTCCCACTCAAGAGAGCATCTGAAAAAGAA 651
Db      3613 GAGGTTCCAAACGAGTGTCCAAAGATGAACTCCCACTCAAGAGAGCATCTGAAAAAGAA 3672
Oy      652  GATGAGGACATTCCTATTCCTTGGCAAGACCTTCTCTATATTAAGAAAGTTCAATT 711
Db      3673 GATGAGGACATTCCTATTCCTTGGCAAGACCTTCTCTATATTAAGAAAGTTCAATT 3732
Oy      712  CATTGGAGAGACACCTTG 731
Db      3733 CATTGGAGAGACACCTTG 3752

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Search completed: June 5, 2006, 05:16:24  
 Job time : 198 secs

18	550	74.7	10339	7	US-10-138-478-13	Sequence 13, Appl
19	548.4	74.5	10160	8	US-10-759-602-68	Sequence 8, Appl
20	548.4	74.5	11784	8	US-10-759-602-9	Sequence 9, Appl
21	548.4	74.5	11591	8	US-10-759-602-10	Sequence 10, Appl
22	545.2	74.1	612	15	US-11-038-98A-1	Sequence 11, Appl
23	543.6	73.9	4149	6	US-10-232-665-13	Sequence 13, Appl
24	543.6	73.9	4149	15	US-11-192-801-13	Sequence 13, Appl
25	543.6	72.6	5767	3	US-09-810-8618-3	Sequence 3, Appl
26	543.6	72.6	5767	3	US-10-792-491-3	Sequence 3, Appl
27	534.6	72.6	5767	3	US-10-792-491-4	Sequence 3, Appl
28	534.6	72.6	14446	6	US-10-792-491-4	Sequence 10, Appl
29	536	71.5	829	6	US-10-109-812-10	Sequence 12, Appl
30	536	71.5	1334	7	US-10-322-656-12	Sequence 2, Appl
31	536	71.5	11478	10	US-10-473-945-2	Sequence 5, Appl
32	536	71.5	12304	10	US-10-473-945-5	Sequence 4, Appl
33	536	71.5	12497	7	US-10-473-945-4	Sequence 4, Appl
34	534	69.8	8428	7	US-10-161-403-90	Sequence 90, Appl
35	534	69.8	8428	9	US-10-161-408-2	Sequence 2, Appl
36	534	69.8	8428	10	US-10-161-408-2	Sequence 90, Appl
37	534	69.8	8428	13	US-11-086-076-90	Sequence 90, Appl
38	534	69.8	10122	16	US-11-082-154A-90	Sequence 97, Appl
39	534	69.8	10122	9	US-10-161-408-8	Sequence 97, Appl
40	534	69.8	10122	10	US-10-161-408-8	Sequence 6, Appl
41	534	69.8	10122	10	US-10-161-408-8	Sequence 6, Appl
42	534	69.8	10122	16	US-11-086-076-97	Sequence 97, Appl
43	534	69.8	10122	16	US-11-082-154A-97	Sequence 97, Appl
44	534	69.8	10549	9	US-10-161-403-92	Sequence 92, Appl
45	534	69.8	10549	9	US-10-161-408-3	Sequence 3, Appl

## RESULT 1

US-10-075-105C-1  
Sequence 1, Application US/10075-105C  
Application No. US20050189432A1  
GEMMA, J. Nathan T.  
GEMMA, J. Nathan T.  
APPLICANT: Gray, Dennis J  
TITLE OF INVENTION: Bi-Directional  
FILE REFERENCE: 7270-72978  
CURRENT APPLICATION NUMBER: US/10/075-105C  
CURRENT FILING DATE: 2002-02-13  
PRIOR APPLICATION NUMBER: 60/268,358  
PRIOR FILING DATE: 2001-02-13  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patent in version 3.1  
SEQ ID NO: 1  
SEQ ID NO: 736  
TYPE: DNA  
ORGANISM: Canv 35S  
FEATURES:  
US-10-075-105C-1

## SUMMARIES

	Query Match	Best Local Similarity	100.0%	Score 736	DB 10	Length 736	
	Best Local Similarity	100.0%	Score 736	DB 10	Length 736		
	Matches 736	Conservative 0	Mismatches 0	Indels 0	Gaps 0		
QY	1	GGATCAGCGTGTCTCTCCAAATGAAATGACATCTCCCTATATAGAGGAAGGCTTCTGGG	60				
DB	1	GGATCAGCGTGTCTCTCCAAATGAAATGACATCTCCCTATATAGAGGAAGGCTTCTGGG	60				
QY	61	AGATCTAGCTGGGATGTGGCGTACTCCCTACTGTGAGGAGATCTGGGAGACTTCTGCG	120				
DB	61	AAAGGATAGTGGGATGTGGCGTACTCCCTACTGTGAGGAGATCTGGGAGACTTCTGCG	120				
QY	121	AGTGAGACTTTTTCACAAAGAGGGTATATCGGGAACACTCTCTCGAGTTCATATGCCCAAGT	180				
DB	121	AGTGAGACTTTTTCACAAAGAGGGTATATCGGGAACACTCTCTCGAGTTCATATGCCCAAGT	180				

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Oy 181 ATCTGCACTTCATCAAAAGGACAGTAAAGAGAGTGGACCTCAAAATGCCATCAT 240
Db 181 ATCTGCACTTCATCAAAAGGACAGTAAAGAGAGTGGACCTCAAAATGCCATCAT 240
Oy 241 TCGAATTAAGAAAGGCTATCTGTCAGATGCTCTGCGCAAGTGTCTCCAAAGTGA 300
Db 241 TCGAATTAAGAAAGGCTATCTGTCAGATGCTCTGCGCAAGTGTCTCCAAAGTGA 300
Oy 301 CCCCCCAAGGAGAGAGTGTGGGAAAAAGAGAGGTTCCAAAGGTTCCAAAGCA 360
Db 301 CCCCCCAAGGAGAGAGTGTGGGAAAAAGAGAGGTTCCAAAGGTTCCAAAGCA 360
Oy 361 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Oy 421 GAATTCATGCTCCAGCTATCTGTCATTCATCAAAAGGACAGTAAAGAGTGGC 480
Db 421 GAATTCATGCTCCAGCTATCTGTCATTCATCAAAAGGACAGTAAAGAGTGGC 480
Oy 481 ACCGCAAAAGGACATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 ACCGCAAAAGGACATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 540
Oy 541 AGTGTCCCAAGAGTGAAGGACCCCAAGGAGAGAGTGTGGGAAAAAGAGTGGC 600
Db 541 AGTGTCCCAAGAGTGAAGGACCCCAAGGAGAGAGTGTGGGAAAAAGAGTGGC 600
Oy 601 ACAGGCTTCGAAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 ACAGGCTTCGAAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Oy 661 CATTCGCACTTCCTGCGAAGAGCCCTTCCTATATAGAGAGTTCATTCATTCAG 720
Db 661 CATTCGCACTTCCTGCGAAGAGCCCTTCCTATATAGAGAGTTCATTCATTCAG 720
Oy 721 AGGACAGCTGATGATCC 736
Db 721 AGGACAGCTGATGATCC 736
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## RESULT 3

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US-10-075-105c-3
Sequence 3: Application US/10075105C
Publication No. US20050188432A1
GENERAL INFORMATION:
APPLICANT: L. L. ZHILIAN T
APPLICANT: GREY, DENNIS J
TITLE OF INVENTION: BI-DIRECTIONAL Dual Promoter Complex with Enhanced Promoter Activity
FILE REFERENCE: 7270-72978
CURRENT FILING DATE: 2002-02-13
PRIORITY FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1360
TYPE: DNA
ORGANISM: CANV 35S
FEATURE:
OTHER INFORMATION:
US-10-075-105c-3
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Query Match 81.3%; Score 597.4; DB 10; Length 1360;
Best Local Similarity 99.8%; Pctd No. 36-101;
Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 109 AGAAGCTTCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 168
Db 762 ATAAAGCTTCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821
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Oy 169 CATTGCCAGCTATCTGCACTTCATCAAAAGGACAGTAAAGAGAGTGGACCTCAAC 228
Db 822 CATTGCCAGCTATCTGCACTTCATCAAAAGGACAGTAAAGAGAGTGGACCTCAAC 881
Oy 229 AATTCATCACTTCGATTAAGAAAGGCTATCTGTCAGATGCTCTGCGCAAGTGTCT 288
Db 882 AATTCATCACTTCGATTAAGAAAGGCTATCTGTCAGATGCTCTGCGCAAGTGTCT 941
Oy 289 CCCCCAAGTGAAGGACCCCAAGGAGAGAGTGTGGGAAAAAGAGAGGTTCCAAAGCA 348
Db 942 CCCCCAAGTGAAGGACCCCAAGGAGAGAGTGTGGGAAAAAGAGAGGTTCCAAAGCA 1001
Oy 349 TCTTCAAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408
Db 1002 TCTTCAAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1061
Oy 409 GGAAGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468
Db 1062 GGAAGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1121
Oy 469 AAGGAGAGTGGACCTCAAAATGCCATGATGATGATGATGATGATGATGATGATGATGAT 528
Db 1122 AAGGAGAGTGGACCTCAAAATGCCATGATGATGATGATGATGATGATGATGATGATGAT 588
Oy 529 GCCTTCGCGACAGTGTCTCCAAAGTGAAGAGTGGACCCCAAGGAGAGAGTGTGGAAAA 588
Db 1182 GCCTTCGCGACAGTGTCTCCAAAGTGAAGAGTGGACCCCAAGGAGAGAGTGTGGAAAA 1241
Oy 589 GAAAGCTTCGAAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
Db 1242 GAAAGCTTCGAAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1301
Oy 649 AGGAGTGAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 707
Db 1302 AGGAGTGAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
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## RESULT 3

```
US-09-943-692-33
Sequence 3: Application US/09943692
Publication No. US20020152496A1
GENERAL INFORMATION:
APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FUCHS, ROY L. B.
APPLICANT: LARVIA, SYLVIA A.
APPLICANT: McPHERSON, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOET:195--1
CURRENT FILING DATE: 2001-08-31
PRIORITY FILING DATE: 09/027, 998
PRIORITY FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 661
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Cauliflower Mosaic Viral Promoter (CANY35S)
US-09-943-692-33
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Query Match 75.3%; Score 554; DB 3; Length 661;
Best Local Similarity 94.5%; Pctd No. 130-176;
Matches 586; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
Oy 116 TCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 175
Db 20 TCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 79
Oy 176 CAGTATCTGCACTTCATCAAAAGGACAGTAAAGAGAGTGGACCTCAAAATGCC 235
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Db 80 CAGCTATCTGTCACTTTATTGTGAGATAGTGGAAAGGAGGTGGCTCTTACAAATGCC 139
Qy 236 ATCAATTCGGATAAAGGAAGGCTATCGTTCAAGATGCTCTTCCGACACAGTGGTCCCAAG 295
Db 140 ATCAATTCGGATAAAGGAAGGCAATCGTTGAGATGCTCTTCCGACACAGTGGTCCCAAG 199
Qy 296 ATGACGCCCCACCCACGAGAGCAATCGTGGAAAGGAAGCAAGTTCGAAACCAAGTCTTCAA 355
Db 200 ATGACGCCCCACCCACGAGAGCAATCGTGGAAAGGAAGCAAGTTCGAAACCAAGTCTTCAA 259
Qy 356 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
Db 260 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 319
Qy 412 AACCTCTCGGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 471
Db 320 AACCTCTCGGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 379
Qy 472 GAAGGTGGCACTCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 531
Db 380 GAAGGTGGCTCTCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 439
Qy 532 TCTGCGGACAGTGGTCCCAAGATGACCCCAAGATGACCCCAAGATGACCCCAAGATGACCCCAAG 591
Db 440 TCTGCGGACAGTGGTCCCAAGATGACCCCAAGATGACCCCAAGATGACCCCAAGATGACCCCAAG 499
Qy 592 GAGCTTCCAAACCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 651
Db 500 GAGCTTCCAAACCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 559
Qy 652 GAGGAGGCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 711
Db 560 GAGGAGGCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 619
Qy 712 CATTTCGAGAGGACACGCTG 731
Db 620 CATTTCGAGAGGACACGCTG 639
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## RESULT 4

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US-10-213-791-29
; Sequence 29, Application US/10213791
; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SIZE: 2107
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expression
; OTHER INFORMATION: cassette comprising plant operable promoter linked
; OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(590)
; NAME/KEY: 5'UTR
; LOCATION: (615)..(605)
; NAME/KEY: intron
; LOCATION: (699)..(1148)
```

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; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1149)..(1426)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1427)..(1858)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1869)..(2102)
; US-10-213-791-29
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## Query Match

Basic Local Similarity 75.3%; Score 554; DB 6; Length 2107;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

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Qy 116 TCTGACGTGAGACTTTTCAACAAGAGGTAATATCGGGAACCTCTCTCGGATTCGATTCGATTCG 175
Db 28 TCCGATGTGAGACTTTTCAACAAGGTAATATATCCGGAACCTCTCTCGGATTCGATTCGATTCG 87
Qy 176 CAGCTATCTGTCACTTTTCAACAAGGACAGTAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 235
Db 88 CAGCTATCTGTCACTTTTATTTGGAAGATAGTGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 147
Qy 236 ATCAATTCGGATTAAGGAAGGCTATCGTTCAAGATGCTCTCTCGGACAGTGGTCCCAAG 295
Db 148 ATCAATTCGGATTAAGGAAGGCTATCGTTCAAGATGCTCTCTCGGACAGTGGTCCCAAG 207
Qy 296 ATGGAGCCCCCACCACGAGGAGCATCGTGGAAAGGAAGAGACCTTCCACACGCTCTTCAA 355
Db 208 ATGGAGCCCCCACCACGAGGAGCATCGTGGAAAGGAAGAGACCTTCCACACGCTCTTCAA 267
Qy 356 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
Db 268 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327
Qy 412 AACCTCTCGGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 471
Db 328 AACCTCTCGGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 387
Qy 472 GAAGGTGGCACTCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 531
Db 388 GAAGGTGGCTCTCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 447
Qy 532 TCTGCGGACAGTGGTCCCAAGATGACCCCAAGATGACCCCAAGATGACCCCAAGATGACCCCAAG 591
Db 448 TCTGCGGACAGTGGTCCCAAGATGACCCCAAGATGACCCCAAGATGACCCCAAGATGACCCCAAG 507
Qy 592 GAGCTTCCAAACCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 651
Db 508 GAGCTTCCAAACCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 567
Qy 652 GATGAGGCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 711
Db 568 GATGAGGCAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 627
Qy 712 CATTTCGAGAGGACACGCTG 731
Db 628 CATTTCGAGAGGACACGCTG 647
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## RESULT 5

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US-10-213-791-25
; Sequence 25, Application US/10213791
; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
```

PRIOR FILING DATE: 1998-11-17  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 25  
LENGTH: 2122  
TYPE: DNA  
FEATURES:  
NAME/KEY: Artificial Sequence  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette comprising plant promoter linked to  
OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked  
OTHER INFORMATION: to termination sequence  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (6)..(620)  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: (643)..(715)  
NAME/KEY: Intron  
LOCATION: (729)..(1178)  
FEATURE:  
NAME/KEY: translat\_peptide  
LOCATION: (1179)..(1406)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1407)..(1838)  
FEATURE:  
NAME/KEY: terminator  
LOCATION: (1849)..(2082)  
US-10-213-791-25

Query Match 75.34; Score 554; DB 6; Length 2122;  
Best Local Similarity 94.51; Pred. No. 2, 4e-176;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

116 TCCTGAGTGAACCTTTCAACAAAGGTATATATCGGAAACCTCTCGATTCATTCGTC 175  
8 TCCTGAGTGAACCTTTCAACAAAGGTATATATCGGAAACCTCTCGATTCATTCGTC 67  
176 CAGCTATCTGCTCACTTCATCAAAAGACATGAGAAAGAGAGTGCACCTTCAATGCC 235  
68 CAGCTATCTGCTCACTTCATCAAAAGACATGAGAAAGAGAGTGCACCTTCAATGCC 127  
236 ATCATTTGGATTAAGAAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 295  
128 ATCATTTGGATTAAGAAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 187  
296 ATGACACCCCAACCAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 355  
188 ATGACACCCCAACCAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 247  
356 AGCAAGTGAATGATGAT---TGCAGTGAACCTTTCAACAAAGGTATATTCGGA 411  
248 AGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307  
412 AACCTCTCGATTCATTCGGAACCTTCAAAAGAGAGTGCACCTTCAATGCC 471  
308 AACCTCTCGATTCATTCGGAACCTTCAAAAGAGAGTGCACCTTCAATGCC 367  
472 GAAAGTGAACCTTCAAAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 531  
368 GAAAGTGAACCTTCAAAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 427  
532 TCTGCGAAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCA 591  
428 TCTGCGAAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCA 487  
592 GACCTTCGAACAGTTCGAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAAG 651  
488 GACCTTCGAACAGTTCGAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAAG 547  
652 GATGACGCAATTCCTTCGGAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCA 711

Db 548 GATGACGCAATTCCTTCGGAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCA 607  
QY 712 CATTGAGAGACACCTTCG 731  
Db 608 CATTGAGAGAGACACCTTC 627

RESULT 6

US-10-213-791-31  
Sequence 31, Application US/10213791  
Publication No. US20030106096A1  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
TITLE OF INVENTION: Phosphonate Metabolizing Plants  
FILE REFERENCE: US-2113503 US/10/213,791  
CURRENT FILING DATE: 2002-08-07  
PRIOR APPLICATION NUMBER: US/09/441,340  
PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 60/108,763  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 31  
LENGTH: 2436  
TYPE: DNA  
FEATURES:  
NAME/KEY: Artificial Sequence  
OTHER INFORMATION: Description of Artificial Sequence:monocot  
OTHER INFORMATION: expression cassette comprising plant operable  
OTHER INFORMATION: promoter linked to an Intron, a sequence coding  
OTHER INFORMATION: for an AMPA acetyltransferase, and a termination  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (26)..(640)  
FEATURE:  
NAME/KEY: Intron  
LOCATION: (670)..(1473)  
NAME/KEY: translat\_peptide  
LOCATION: (1498)..(1725)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1726)..(2157)  
FEATURE:  
NAME/KEY: terminator  
LOCATION: (2172)..(2427)  
US-10-213-791-31

Query Match 75.34; Score 554; DB 6; Length 2436;  
Best Local Similarity 94.51; Pred. No. 2, 4e-176;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

116 TCCTGAGTGAACCTTTCAACAAAGGTATATATCGGAAACCTCTCGATTCATTCGTC 175  
28 TCCTGAGTGAACCTTTCAACAAAGGTATATATCGGAAACCTCTCGATTCATTCGTC 87  
176 CAGCTATCTGCTCACTTCATCAAAAGACATGAGAAAGAGAGTGCACCTTCAATGCC 235  
88 CAGCTATCTGCTCACTTCATCAAAAGACATGAGAAAGAGAGTGCACCTTCAATGCC 147  
236 ATCATTTGGATTAAGAAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 295  
148 ATCATTTGGATTAAGAAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 207  
296 ATGACACCCCAACCAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 355  
208 ATGACACCCCAACCAAGAGAGTGCACCTTCAAAAGAGAGTGCACCTTCAATGCC 287  
356 AGCAAGTGAATGATGAT---TGCAGTGAACCTTTCAACAAAGGTATATTCGGA 411



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Db 28 TCCGATGTGAGACTTTTCACAAAGGATATTCGGAAACCTCTCGATTCATTCATTCGCC 87
Oy 176 CAGCTATCTGCTCATCTTCATCAAAAGACATGAGAAAGAGAGTGGCACTTCAAAATGCC 235
Db 88 CAGCTATCTGCTCATCTTCATCAAAAGACATGAGAAAGAGAGTGGCACTTCAAAATGCC 147
Oy 236 ATGATGCGATTAAGAAAGGCTATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 295
Db 148 ATGATGCGATTAAGAAAGGCTATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
Oy 296 ATGAGACCCCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 355
Db 208 ATGAGACCCCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267
Oy 356 AGCAAGTGAATTGATGTAT---TGCAGTGAAGCTTTTCACAAAGGATATTCGGCA 411
Db 266 AGCAAGTGAATTGATGTATGTGATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
Oy 412 AACCTCTCGATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 471
Db 328 AACCTCTCGATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
Oy 472 GAAGTGGCACTTCAAAATGCAATTCGATTAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 531
Db 388 GAAGTGGCACTTCAAAATGCAATTCGATTAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 447
Oy 532 TCTGCGACAGTGTGCTCCAAAGATGAGACCCCAACCAAGAGAGAGAGAGAGAGAGAG 591
Db 448 TCTGCGACAGTGTGCTCCAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 507
Oy 592 GAGCTTCCAAACAGCTCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 651
Db 508 GAGCTTCCAAACAGCTCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 567
Oy 652 GATGAGGCAATCCCATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 711
Db 568 GATGAGGCAATCCCATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 627
Oy 712 CATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
Db 628 CATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 647
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## RESULT 9

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US-11-192-801-23
Sequence 23, Application US/11192801
Publication No. US20050273882A1
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192,801
PRIORITY NUMBER: US/01/232,665
PRIORITY FILING DATE: 2002-08-29
PRIORITY FILING DATE: 1999-08-19
PRIORITY FILING DATE: 1999-08-19
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 23
LENGTH: 3469
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette
NAME/KEY: Promoter
LOCATION: (25)..(640)
OTHER INFORMATION: P-CMV,35S
FEATURE:
NAME/KEY: 5'-UTR
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LOCATION: (664)..(734)
OTHER INFORMATION: L-Ta, hcb1
FEATURE:
NAME/KEY: Intron
LOCATION: (748)..(1238)
OTHER INFORMATION: T-08, hcb1
NAME/KEY: CDS
LOCATION: (1241)..(3199)
OTHER INFORMATION: Cry3Bb1 variant 11231mw2
FEATURE:
NAME/KEY: terminator
LOCATION: (3217)..(3450)
OTHER INFORMATION: T-Ta, hnp17
US-11-192-801-23
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Query Match 75.3%, Score 554, DB 15, Length 3469;  
Best Local Similarity 94.5%, Fred. No. 3.8e-17;  
Matches 586, Conservative 0, Mismatches 30, Indels 4, Gaps 1.

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Oy 116 TCTGCAATGAGAGCTTTTCACAAAGGATATTCGGAAACCTCTCGATTCATTCATTCGCC 175
Db 28 TCCGATGTGAGACTTTTCACAAAGGATATTCGGAAACCTCTCGATTCATTCATTCGCC 87
Oy 176 CAGCTATCTGCTCATCTTCATCAAAAGACATGAGAAAGAGAGTGGCACTTCAAAATGCC 235
Db 88 CAGCTATCTGCTCATCTTCATCAAAAGACATGAGAAAGAGAGTGGCACTTCAAAATGCC 147
Oy 236 ATGATGCGATTAAGAAAGGCTATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 295
Db 148 ATGATGCGATTAAGAAAGGCTATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
Oy 296 ATGAGACCCCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 355
Db 208 ATGAGACCCCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267
Oy 356 AGCAAGTGAATTGATGTAT---TGCAGTGAAGCTTTTCACAAAGGATATTCGGCA 411
Db 266 AGCAAGTGAATTGATGTATGTGATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
Oy 412 AACCTCTCGATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 471
Db 328 AACCTCTCGATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
Oy 472 GAAGTGGCACTTCAAAATGCAATTCGATTAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 531
Db 388 GAAGTGGCACTTCAAAATGCAATTCGATTAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 447
Oy 532 TCTGCGACAGTGTGCTCCAAAGATGAGACCCCAACCAAGAGAGAGAGAGAGAGAGAG 591
Db 448 TCTGCGACAGTGTGCTCCAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 507
Oy 592 GAGCTTCCAAACAGCTCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 651
Db 508 GAGCTTCCAAACAGCTCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 567
Oy 652 GATGAGGCAATCCCATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 711
Db 568 GATGAGGCAATCCCATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 627
Oy 712 CATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
Db 628 CATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 647
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## RESULT 10

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US-10-232-665-15
Sequence 15, Application US/10232665
Publication No. US2003015630A1
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
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/ CURRENT APPLICATION NUMBER: US/10/232,665  
 / CURRENT FILING DATE: 2002-08-29  
 / PRIOR APPLICATION NUMBER: US/09/377,466  
 / NUMBER OF SEQ ID NOS: 43  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO: 15  
 / LENGTH: 3754  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Description of Artificial Sequence: expression  
 / OTHER INFORMATION: cassette  
 / FEATURE:  
 / NAME/KEY: promoter  
 / LOCATION: (25)..(640)  
 / OTHER INFORMATION: P-CaMV.35S  
 / FEATURE:  
 / NAME/KEY: intron  
 / LOCATION: (659)..  
 / OTHER INFORMATION: I-Zm.Hsp70  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: (1490)..(3448)  
 / OTHER INFORMATION: Cry3Bb1 variant v11231  
 / FEATURE:  
 / NAME/KEY: terminator  
 / LOCATION: (3475)..(3730)  
 / OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription  
 / OTHER INFORMATION: termination and polyadenylation sequence  
 / US-10-232-665-15

Query Match 75.3%; Score 554; DB 6; Length 3754;  
 Best Local Similarity 94.5%; Pred. No. 3,2e-176;  
 Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;  
 QY 116 TCTGCACTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC 175  
 DB 28 TCCGATGTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC 87  
 QY 176 CAGCTATCTGCTACTTCATCAAAAGGACAGTAGAGAAAGGAGGTGGACCTACAAATGCC 235  
 DB 88 CAGCTATCTGCTACTTCATCAAAAGGAGTAAATATCGGAAACCTCTCGGATTCATTGCC 147  
 QY 236 ATGAGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 387  
 DB 328 AACCTCTCGGATTCATTCGCGAGCTATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 531  
 QY 472 GAGGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 591  
 DB 388 GAGGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 447  
 QY 532 TCTGCGGACAGTGGTCCCAAGAGTGGACCCCAACGAGGAGGAGGTATCTCGGATTCATTGCC 591  
 DB 448 TCTGCGGACAGTGGTCCCAAGAGTGGACCCCAACGAGGAGGAGGTATCTCGGATTCATTGCC 507  
 QY 592 GAGGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 651  
 DB 508 GAGGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 567  
 QY 652 GATGAGGACATCCCACTCTCTCGGAGGAGGAGGTATCTCGGATTCATTGCC 711

DB 568 TCTGCACTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC 627  
 QY 712 CATTGGAGAGACACGCTG 731  
 DB 628 CATTGGAGAGACACGCTG 647

## RESULT 11

US-11-192-801-15  
 / Sequence 15, Application US/11/192801  
 / GENERAL INFORMATION: Charles P.  
 / APPLICANT: Romano  
 / TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
 / FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
 / CURRENT APPLICATION NUMBER: US/11/192,801  
 / CURRENT FILING DATE: 2005-07-29  
 / PRIOR APPLICATION NUMBER: US/10/232,665  
 / PRIOR FILING DATE: 2002-08-29  
 / PRIOR APPLICATION NUMBER: US/09/377,466  
 / PRIOR FILING DATE: 1999-08-19  
 / NUMBER OF SEQ ID NOS: 43  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO: 15  
 / LENGTH: 3754  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Description of Artificial Sequence: expression  
 / OTHER INFORMATION: cassette  
 / FEATURE:  
 / NAME/KEY: promoter  
 / LOCATION: (25)..(640)  
 / OTHER INFORMATION: P-CaMV.35S  
 / FEATURE:  
 / NAME/KEY: intron  
 / LOCATION: (659)..  
 / OTHER INFORMATION: I-Zm.Hsp70  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: (1490)..(3448)  
 / OTHER INFORMATION: Cry3Bb1 variant v11231  
 / FEATURE:  
 / NAME/KEY: terminator  
 / LOCATION: (3475)..(3730)  
 / OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription  
 / OTHER INFORMATION: termination and polyadenylation sequence  
 / US-11-192-801-15

Query Match 75.3%; Score 554; DB 15; Length 3754;  
 Best Local Similarity 94.5%; Pred. No. 3,2e-176;  
 Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;  
 QY 116 TCTGCACTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC 175  
 DB 28 TCCGATGTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC 87  
 QY 176 CAGCTATCTGCTACTTCATCAAAAGGACAGTAGAGAAAGGAGGTGGACCTACAAATGCC 235  
 DB 88 CAGCTATCTGCTACTTCATCAAAAGGAGTAAATATCGGAAACCTCTCGGATTCATTGCC 147  
 QY 236 ATGAGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 387  
 DB 328 AACCTCTCGGATTCATTCGCGAGCTATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 531  
 QY 472 GAGGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 591  
 DB 388 GAGGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 447  
 QY 532 TCTGCGGACAGTGGTCCCAAGAGTGGACCCCAACGAGGAGGAGGTATCTCGGATTCATTGCC 591  
 DB 448 TCTGCGGACAGTGGTCCCAAGAGTGGACCCCAACGAGGAGGAGGTATCTCGGATTCATTGCC 507  
 QY 592 GAGGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 651  
 DB 508 GAGGTGGACCTTCAAAATGCCATCTGCTCAATGAGGAGGAGGTATCTCGGATTCATTGCC 567  
 QY 652 GATGAGGACATCCCACTCTCTCGGAGGAGGAGGTATCTCGGATTCATTGCC 711

Qy	412	AACCTCCCTGGATTCATCATTTGGCCACATATCTCACTCATCAAAAGACAGTGGAAAAG	471
Db	328	AACTCTGATGATTCATCATTTGGCCACATATCTCACTCATCAAAAGACAGTGGAAAAG	387
Qy	472	GAAGGTGGACGCTCAATATGCGCATATGGCAATATAGAAAGAGCTGTATGGTAAATGGC	531
Db	388	GAAGGTGGCTCTCAATATGCGCATATGGCAATATAGAAAGAGCTGTATAGATGGC	447
Qy	532	TCTGCGCAACAGTGTCCCAAGATGGAACCCCACTCCAGAGAGCATGTGGAAAAAGA	591
Db	448	TCTGCGCAACAGTGTCCCAAGATGGAACCCCACTCCAGAGAGCATGTGGAAAAAGA	507
Qy	592	GAGCTTCCAAACAAGCTTCAAAAGACATGATATGATATATCTCACTGAAGTAAAG	651
Db	508	GAGCTTCCAAACAAGCTTCAAAAGACATGATATGATATATCTCACTGAAGTAAAG	567
Qy	652	GATGACGACATCCCACTTCTCTGGCAAGAGCTTCTCTCATATAGCAAGTTCATT	711
Db	568	GATGACGACATCCCACTTCTCTGGCAAGAGCTTCTCTCATATAGCAAGTTCATT	627
Qy	712	CATTGGAGAGGACAGCGTGG	721
Db	628	CATTGGAGAGGACAGCGTGG	647

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RESULT 12
US-10-198-478-16
Sequence 16, Application US/10198478
Publication No. US20030188336x1
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
INVENTOR: Corbin, David R.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endocannabinoid Receptors
FILE REFERENCE: 38-21 (13597) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/186, 002
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 8349
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: completely synthesized
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(8349)
OTHER INFORMATION:
US-10-198-478-16

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	Query Match	Similarity	Score	DB 7	Length
Best Local	95.3%		554	DB 7	8349
Matches	586	Conservative	0	Mismatches	30
				Indels	4
				Gaps	1

[illegible]

RESULT 13  
 US-10-378-810-2/c  
 Sequence 2, Application US/10378810  
 INVENTOR: SMITH, KALLEY A.  
 MAILING ADDRESS: 000302135069XA1  
 COUNTRY OF ORIGIN: INFORMATION  
 APPLICANT: Smith, KalleY A.  
 TITLE OF INVENTION: PROMOTER AND INTRON FROM MAIZE ACTIN DEPOLYMERIZING  
 TITLE OF INVENTION: FACTOR  
 FILE REFERENCE: 50695  
 CURRENT FILING DATE: 2003-03-04 NUMBER: US/03/788,810  
 PRIOR APPLICATION NUMBER: 2003-03-04  
 PRIOR FILING DATE: 1999-11-23  
 NUMBER OF SEQ ID NOS: 2  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO. 2  
 SEQ ID NO. 2  
 SEQ ID NO. 2  
 TYPE: DNA  
 TYPE: DNA  
 TYPE: DNA  
 FEATURE:  
 ORGANISM: Artificial Sequence  
 OTHER INFORMATION: Description of Artificial Sequence: pDAB305  
 US-10-378-810-2

	Query Match	Best Local Similarity	79.2%;	Score 551.1;	DB 7;	Length 5796;
	Matches 588;	Conservative	0;	Mismatches 41;	Indels 2;	Gaps 1;
Qy	105	CTCCAGAGACCTTCGACGTAGACCTTTCAACAAAGGTATATCGGAAACCTCTCTCG	164			
Db	3550	CTGCAGATCTGCAGTCGGGTGGAGACCTTCAACAAAGGTATATCGGAAACCTCTCTCG	3491			
Qy	165	ATTCAATATTCGACGACCTTCACTTCGATCGAAGACGTGTGAAAGAGGTGAC	224			
Db	3490	ATTCAATTCGACGACCTTCTGCACTTATGTGAAAGATGTGAAAGAGAGGTGGCTC	3431			
Qy	225	CTACAAATGCATCATTCGATTAAGGAAAGGCTATCGTCAAGTCCCTCTGCGACAG	284			
Db	3430	CTACAAATGCATCATTCGATTAAGGAAAGGCGCATCTTGAAAGTCCCTCTGCGACAG	3372			
Qy	285	TGGTCCCAAGATGACCCCTCACACGACGATCTGTGAAAGAAAGAGAGCTTCAC	344			
Db	3370	TGGTCCCAAGATGACCCCTCACACGACGAGATCTGTGAAAGAAAGAGAGCTTCAC	3311			



CITY: Indianapolis  
STATE: Indiana  
COUNTRY: USA  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SERIAL: 134513  
CURRENT APPLICATION DATA:  
FILING DATE: 16-Jan-2004  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kraus, Eric J  
TELEPHONE: 317 337 5110  
TELEFAX: 317 337 4847  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-759-602-19

Query Match 74.8%; Score 550.4; DB: Length 9335;  
Best Local Similarity 93.2%; Pred. No. 8.6e-175;  
Matches 587; Conservative 0; Mismatches 41; Indels 2; Gaps 1;  
QY 106 TCGAGAACTTCGACATGAGCTTTCGACAAAGGTAATGCGAAACCTCTGGA 165  
DB 4852 TCGAGATCGATGAGGAGCTTTCGACAAAGGTAATGCGAAACCTCTGGA 4911  
QY 166 TTCATTCGCCAGCTATCTGTCATCTCAATCAAGAGAGAGTAAAGAGGTCAC 225  
DB 4912 TTCATTCGCCAGCTATCTGTCATCTCAATCAAGAGAGAGTAAAGAGGTCAC 4971  
QY 226 TACAATGCCATGATTCGATTAAGAAAGGCTATCTCAAGATCCTTCGCAAGT 285  
DB 4972 TACAATGCCATGATTCGATTAAGAAAGGCTATCTCAAGATCCTTCGCAAGT 5031  
QY 286 GGTCCGAAAG 345  
DB 5032 GGTCCGAAAG 5091  
QY 346 AGCTCTTCAAG 403  
DB 5092 AGCTCTTCAAG 5151  
QY 404 TATCGGAAACCTCTGGAATTCATTCGATTCGATTCGATTCGATTCGATTCG 463  
DB 5152 TATCGGAAACCTCTGGAATTCATTCGATTCGATTCGATTCGATTCGATTCG 5211  
QY 464 TAGAAAG 523  
DB 5212 TAGAAAG 5271  
QY 524 AAGATGCTCTGCGAG 583  
DB 5272 AAGATGCTCTGCGAG 5331  
QY 584 AAAAAG 643  
DB 5332 AAAAAG 5391  
QY 644 AGCTAAG 703  
DB 5392 AGCTAAG 5451  
QY 704 GTTCATTTCATTGAG 733

DB 5452 GTTCATTTCATTGAG 5481  
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Job time: 1300 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 06:00:44 ; Search time 28 Seconds  
(without alignments)  
3095.773 Million cell updates/sec

Title: US-10-075-105C-1  
Perfect score: 736  
Sequence: 1 ggaaccagcgtgctctcc.....ggagagacacgtggatcc 736

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 5886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published Applications NA New:

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq\*
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- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US40\_NEW\_PUB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	554	75.3	5170	6	US-10-525-318-11
2	554	75.3	5600	6	US-10-525-318-11
3	505.2	68.6	7525	7	US-11-248-986-29
4	505.2	68.6	12125	7	US-11-248-986-30
5	342.6	46.5	8810	7	US-11-258-704-40
6	342.6	46.5	8819	7	US-11-258-704-41
7	279.6	38.0	6600	6	US-10-525-318-5
8	279.6	38.0	7000	6	US-10-525-318-8
9	253.4	34.4	2574	7	US-11-248-986-31
10	253.4	34.4	6829	6	US-10-523-290-7
11	242	32.9	508	6	US-10-523-290-7
12	242	32.9	5170	6	US-10-525-318-11
13	99.2	13.5	5600	6	US-10-525-318-11
14	99.2	13.5	5600	6	US-10-525-318-11
15	98.8	13.4	8810	7	US-11-258-704-41
16	98.8	13.4	8819	7	US-11-258-704-41
17	96.4	13.1	7525	7	US-11-248-986-29
18	96.4	13.1	12125	7	US-11-248-986-30
19	85.4	11.6	6600	6	US-10-525-318-5
20	85.4	11.6	7000	6	US-10-525-318-8
21	49	6.7	266	6	US-10-523-290-7
22	49	6.7	508	6	US-10-523-290-3
23	32.8	4.5	612	7	US-11-217-529-81202
24	32.8	4.5	516	7	US-11-217-529-81202
25	30.2	4.1	2880	7	US-11-217-529-78074

## SUMMARIES

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27 29.8 4.0 3409 7 US-11-106-014-93  
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## ALIGNMENTS

RESULT 1  
US-10-525-318-11  
US-10-525-318-11  
Sequence 11, Application US/10525318  
Publication No. US20060112447A1  
GENERAL INFORMATION:  
APPLICANT: Monsanto Technology LLC  
APPLICANT: Monsanto, Charles P  
APPLICANT: Bogdanova, Natalia N  
TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expression  
FILE REFERENCE: 38-21(15414)  
CURRENT APPLICATION NUMBER: US/10/525,318  
CURRENT FILING DATE: 2005-02-23  
PRIORITY FILING DATE: 2003-08-29  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 11  
LENGTH: 5170  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fully synthetic expression cassette  
NAME/KEY: Promoter  
LOCATION: 156..(640)  
OTHER INFORMATION: P-e35S  
NAME/KEY: 5'UTR  
LOCATION: (665)..(735)  
OTHER INFORMATION: L-Ta.CAB  
FEATURE:  
NAME/KEY: Intron  
LOCATION: (749)..(1239)  
OTHER INFORMATION: I-Os.ACT1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1241..(4930)  
OTHER INFORMATION: Cry1Bb variant  
FEATURE:  
NAME/KEY: transcription termination\_sequence  
LOCATION: (4931)..(4936)  
OTHER INFORMATION: miscellaneous  
FEATURE:  
NAME/KEY: polyadenylation sequence  
LOCATION: (4937)..(5170)  
OTHER INFORMATION: T-Ta.hsp70  
US-10-525-318-11

Query Match 75.3%; Score 554; DB 6; Length 5170;  
Best Local Similarity 94.3%; Fred No. 46-173;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Oy 116 TCTGCACTGAGCTTTTCAAGAGGTAATTCGGAAACCTCGGATTCATTCGCC 175  
Db TCCGATGAGAGCTTTTCAAGAGGTAATTCGGAAACCTCGGATTCATTCGCC 87

Oy 176 CAGCTATCTGCTCATCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 235  
Db CAGCTATCTGCTCATCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147

Oy 236 ATCATTTGCAATTAAGAAAGGCTATGCTTCAAGAGAGAGAGAGAGAGAGAGAG 295  
Db ATCATTTGCAATTAAGAAAGGCTATGCTTCAAGAGAGAGAGAGAGAGAGAGAG 207

Oy 296 ATGAGACCCCAAG 355  
Db ATGAGACCCCAAG 267

Oy 356 AGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411  
Db AGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327

Oy 412 AACCTCTGCAATTCATTCGCCAGAGCTTCTGCACTTCATCAAAAGAGAGAGAG 471  
Db AACCTCTGCAATTCATTCGCCAGAGCTTCTGCACTTCATCAAAAGAGAGAGAG 447

Oy 472 GAGAGTGGCACTTCAATTCGCCAGAGCTTCTGCACTTCATCAAAAGAGAGAG 531  
Db GAGAGTGGCACTTCAATTCGCCAGAGCTTCTGCACTTCATCAAAAGAGAGAG 387

Oy 532 TCTGCGCAG 591  
Db TCTGCGCAG 507

Oy 592 GAGCTTCAACCAAGCTTTCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 651  
Db GAGCTTCAACCAAGCTTTCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 567

Oy 652 GATGAG 711  
Db GATGAG 627

Oy 712 CATTTGAG 731  
Db CATTTGAG 647

RESULT 2  
US-10-525-318-13  
Sequence 13; Application US/1055318  
General Information  
APPLICANT: Monanto Technology LLC  
APPLICANT: Romano, Natalia N  
TITLE OF INVENTION: Nucleotide Sequences Encoding Cx1B Proteins for Enhanced Expression  
FILE REFERENCE: 38-2115414  
CURRENT FILING DATE: 2005-07-23  
PRIORITY DATE: 2005-07-23  
PRIORITY NUMBER: 60/407,428  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent version 3.1  
SEQ ID NO 13  
LENGTH: 5600  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fully synthetic expression cassette

FEATURE:  
NAME/KEY: promoter  
LOCATION: (26)..(640)  
OTHER INFORMATION: P-635S  
NAME/KEY: 5'UTR  
LOCATION: (665)..(735)  
OTHER INFORMATION: L-Tr, CAB  
FEATURE:  
NAME/KEY: Intron  
LOCATION: (749)..(1239)  
OTHER INFORMATION: I-06, ACT1  
FEATURE:  
NAME/KEY: Transic peptide  
LOCATION: (1255)..(1401)  
OTHER INFORMATION: TP-2m, rbc8  
NAME/KEY: Intron  
LOCATION: (1402)..(1564)  
OTHER INFORMATION: I-2m, rbc8  
FEATURE:  
NAME/KEY: transic peptide  
LOCATION: (1565)..(1651)  
OTHER INFORMATION: TP-2m, rbc8  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1652)..(5341)  
OTHER INFORMATION: Cx1B variant  
FEATURE:  
NAME/KEY: transcription termination sequence  
LOCATION: (5342)..(5347)  
OTHER INFORMATION: miscellaneus  
FEATURE:  
NAME/KEY: polyadenylation sequence  
LOCATION: (5350)..(5592)  
OTHER INFORMATION: T-08, LDH  
US-10-525-318-13

Query Match 75.3%; Score 554; DB 6; Length 5600;  
Best Local Similarity 94.3%; Fred No. 46-173;  
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Oy 116 TCTGCACTGAGCTTTTCAAGAGGTAATTCGGAAACCTCGGATTCATTCGCC 175  
Db TCCGATGAGAGCTTTTCAAGAGGTAATTCGGAAACCTCGGATTCATTCGCC 87

Oy 176 CAGCTATCTGCTCATCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 235  
Db CAGCTATCTGCTCATCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147

Oy 236 ATCATTTGCAATTAAGAAAGGCTATGCTTCAAGAGAGAGAGAGAGAGAGAGAG 295  
Db ATCATTTGCAATTAAGAAAGGCTATGCTTCAAGAGAGAGAGAGAGAGAGAGAG 207

Oy 296 ATGAGACCCCAAG 355  
Db ATGAGACCCCAAG 267

Oy 356 AGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411  
Db AGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327

Oy 412 AACCTCTGCAATTCATTCGCCAGAGCTTCTGCACTTCATCAAAAGAGAGAGAG 471  
Db AACCTCTGCAATTCATTCGCCAGAGCTTCTGCACTTCATCAAAAGAGAGAGAG 447

Oy 472 GAGAGTGGCACTTCAATTCGCCAGAGCTTCTGCACTTCATCAAAAGAGAGAG 531  
Db GAGAGTGGCACTTCAATTCGCCAGAGCTTCTGCACTTCATCAAAAGAGAGAG 387

Oy 532 TCTGCGCAG 591  
Db TCTGCGCAG 507

QY 592 GACGTTCCACCAACCTCTTCAAGCAAGTGGATTGATGATATCTCACTGACGTAAAG 651  
 DB 508 GACGTTCCACCAACCTCTTCAAGCAAGTGGATTGATGATATCTCACTGACGTAAAG 567  
 QY 652 GATGAGCAGCAATCCCACTATCTTCCGACAGCCCTCTCTCTATATAGAGAACTGATTT 711  
 DB 568 GATGAGCAGCAATCCCACTATCTTCCGACAGCCCTCTCTCTATATAGAGAACTGATTT 627  
 QY 712 CATTTGGAGAGACACGCTG 731  
 DB 628 CATTTGGAGAGACACGCTG 647

## RESULT 3

US-11-248-986-29  
 ; Sequence 29, Application US/11248986  
 ; Publication No. US20060112448A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OSBOURN, ANNE E.  
 ; TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS  
 ; FILE REFERENCE: BB1550 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/248,986  
 ; CURRENT FILING DATE: 2005-10-12  
 ; PRIOR APPLICATION NUMBER: 60/619,203  
 ; PRIOR FILING DATE: 2004-10-15  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO: 29  
 ; LENGTH: 7525  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Maize recombinant DNA construct 1  
 US-11-248-986-29

Query Match 68.6%; Score 505.2; DB 7; Length 7525;  
 Best Local Similarity 86.7%; Pred. No. 6.2e-157;  
 Matches 605; Conservative 0; Mismatches 8; Indels 85; Gaps 1;

QY 121 AGTGAGACTTTTCAACAAAGGCTAATTCGGGAACCTCTCCGATTCCTGCCAGCT 180  
 DB 5142 ATTGAGACTTTTCAACAAAGGCTAATTCGGGAACCTCTCCGATTCCTGCCAGCT 5201  
 QY 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAGAGGTGGCACTTCAAAATGCCATCAT 240  
 DB 5202 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAGAGGTGGCACTTCAAAATGCCATCAT 5261  
 QY 241 TCGATTAAGGAAGGCTATCTTCAAGATGCTCTCCGACAGTGGTCCCAAGATGGA 300  
 DB 5262 TCGATTAAGGAAGGCTATCTTCAAGATGCTCTCCGACAGTGGTCCCAAGATGGA 5321  
 QY 301 CCCCACCCACGAGGAGCATCTGTGGAAAAGAGAGGTTCACACACATCTTCAAGAGCA 360  
 DB 5322 CCCCACCCACGAGGAGCATCTGTGGAAAAGAGAGGTTCACACACATCTTCAAGAGCA 5381  
 QY 361 GTGGATTGATGTGAT----- 375  
 DB 5382 GTGGATTGATGTGATCTCTAGAAATCCGTCAACATGGTGGAGACGACACTCTCGTCTA 5441  
 QY 376 -----TGCAGTGAGACTTTTCAACA 395  
 DB 5442 CTCGAAGATATCAAGATACAGTCTCAGAGAACAAGGGCTATTGAGACTTTTCAACA 5501  
 QY 396 AAGGTAATATCGGGAACCTCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCATCAA 455  
 DB 5502 AAGGTAATATCGGGAACCTCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCATCAA 5561  
 QY 456 AAGGACACTAGAAAGGAGGTGGCACTCAAAATGCCATCTGTGGATTAAGGAAGGC 515  
 DB 5562 AAGGACACTAGAAAGGAGGTGGCACTCAAAATGCCATCTGTGGATTAAGGAAGGC 5621

QY 516 TATCGTTCAAGATGCTCTCCGACAGTGGTCCCAAGATGAGCCCCACCCACGAGGAG 575  
 DB 5622 TATCGTTCAAGATGCTCTCCGACAGTGGTCCCAAGATGAGCCCCACCCACGAGGAG 5681  
 QY 576 CATCTGGAAAAAGAGAGCTTCCAAACCACTCTCTTCAAGCAAGTGGATTGATGATAT 635  
 DB 5682 CATCTGGAAAAAGAGAGCTTCCAAACCACTCTCTTCAAGCAAGTGGATTGATGATAT 5741  
 QY 636 CTCACCTGACGTAGAGATGAGCAACCTGCACTATCTCTTCCGAGACCTTCTCTAT 695  
 DB 5742 CTCACCTGACGTAGAGATGAGCAACCTGCACTATCTCTTCCGAGACCTTCTCTAT 5801  
 QY 696 ATAAGGAAGTTCATTTTCATTTGGAGAGACACGCTGGA 733  
 DB 5802 ATAAGGAAGTTCATTTTCATTTGGAGAGACACGCTGCA 5839

## RESULT 4

US-11-248-986-30  
 ; Sequence 30, Application US/11248986  
 ; Publication No. US20060112448A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OSBOURN, ANNE E.  
 ; TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS  
 ; FILE REFERENCE: BB1550 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/248,986  
 ; CURRENT FILING DATE: 2005-10-12  
 ; PRIOR APPLICATION NUMBER: 60/619,203  
 ; PRIOR FILING DATE: 2004-10-15  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO: 30  
 ; LENGTH: 12125  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: maize recombinant DNA construct 2  
 US-11-248-986-30

Query Match 68.6%; Score 505.2; DB 7; Length 12125;  
 Best Local Similarity 86.7%; Pred. No. 7.9e-157;  
 Matches 605; Conservative 0; Mismatches 8; Indels 85; Gaps 1;

QY 121 AGTGAGACTTTTCAACAAAGGCTAATTCGGGAACCTCTCCGATTCCTGCCAGCT 180  
 DB 9742 ATTGAGACTTTTCAACAAAGGCTAATTCGGGAACCTCTCCGATTCCTGCCAGCT 9801  
 QY 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAGAGGTGGCACTTCAAAATGCCATCAT 240  
 DB 9802 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAGAGGTGGCACTTCAAAATGCCATCAT 9861  
 QY 241 TCGATTAAGGAAGGCTATCTTCAAGATGCTCTCCGACAGTGGTCCCAAGATGGA 300  
 DB 9862 TCGATTAAGGAAGGCTATCTTCAAGATGCTCTCCGACAGTGGTCCCAAGATGGA 9921  
 QY 301 CCCCACCCACGAGGAGCATCTGTGGAAAAGAGAGGTTCACACAGTCTTCAAGAGCA 360  
 DB 9922 CCCCACCCACGAGGAGCATCTGTGGAAAAGAGAGGTTCACACAGTCTTCAAGAGCA 9981  
 QY 361 GTGGATTGATGTGAT----- 375  
 DB 9982 GTGGATTGATGTGATCTCTAGAAATCCGTCAACATGGTGGAGACGACACTCTCGTCTA 10041  
 QY 376 -----TGCAGTGAGACTTTTCAACA 395  
 DB 10042 CTCGAAGATATCAAGATACAGTCTCAGAGAACAAGGGCTATTGAGACTTTTCAACA 10101  
 QY 396 AAGGTAATATCGGGAACCTCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCATCAA 455  
 DB 10102 AAGGTAATATCGGGAACCTCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCATCAA 10161  
 QY 456 AAGGACACTAGAAAGGAGGTGGCACTCAAAATGCCATCTGTGGATTAAGGAAGGC 515





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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fully synthetic expression cassette
; NAME/KEY: Promoter
; LOCATION: (174)..(490)
; OTHER INFORMATION: P-CMV 35S
; NAME/KEY: CDS
; LOCATION: (526)..(1320)
; OTHER INFORMATION: npfII
; NAME/KEY: transcription termination & polyadenylation sequence
; LOCATION: (1315)..(1767)
; OTHER INFORMATION: T-AGRTu.nos3'
; NAME/KEY: Promoter
; LOCATION: (1809)..(2386)
; OTHER INFORMATION: P-FMV
; NAME/KEY: 5' untranslated leader
; LOCATION: (2407)..(2480)
; OTHER INFORMATION: L-Os.betabubulin
; NAME/KEY: Intron
; LOCATION: (2498)..(2614)
; OTHER INFORMATION: I-Os.PAL
; NAME/KEY: CDS
; LOCATION: (2644)..(6333)
; OTHER INFORMATION: CryIbB variant
; NAME/KEY: transcription termination & polyadenylation sequence
; LOCATION: (6345)..(6584)
; OTHER INFORMATION: T-Os.LDH
US-10-525-318-5

Query Match
Best Local Similarity 38.0%; Score 279.6; DB 6; Length 6600;
Matches 293; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 437 CTATCTGTCACTTCAATCAAAAGGACAGTGAAGAGGAGTGCACCTACAAATGCCATC 496
DB 174 CTATCTGTCACTTCAATCAAAAGGACAGTGAAGAGGAGTGCACCTACAAATGCCATC 233

QY 497 AFTGGCATTAAGAAAGGCTATCGTTCAAGATGCTCTGCCAGACGTGTCCAAAGATG 556
DB 234 AFTGGCATTAAGAAAGGCTATCGTTCAAGATGCTCTGCCAGACGTGTCCAAAGATG 293

QY 557 GACCCGACCCAGAGGAGCTGTGGAAAGAGAGTTCACACCAAGTTCCTTCAAGC 616
DB 294 GACCCGACCCAGAGGAGCTGTGGAAAGAGAGTTCACACCAAGTTCCTTCAAGC 353

QY 617 AAGTGGATTGATGATCTCCACTGACCTAAGG-ATGACGCAATCCCACTATCT 675
DB 354 AAGTGGATTGATGATCTCCACTGACCTAAGG-ATGACGCAATCCCACTATCT 413

QY 676 TCGCAGAGCCCTTCTCTATATAGGAAGTTCATTTCTTTGGAGGAGCAGCTGGA 733
DB 414 TCGCAGAGCCCTTCTCTATATAGGAAGTTCATTTCTTTGGAGGAGCAGCTGGA 471

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RESULT 8
US-10-525-318-8
; Publication US/10525318
; Publication No.US2006012447A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Romano, Charles P

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; APPLICANT: Bogdanova, Natalia N
; TITLE OF INVENTION: Nucleotide Sequences Encoding CryIbB Proteins for Enhanced Expre:
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15414)
; CURRENT APPLICATION NUMBER: US/10/525,318
; PRIOR FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: 60/407,428
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO. 8
; LENGTH: 7000
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fully synthetic expression cassette
; NAME/KEY: promoter
; LOCATION: (174)..(490)
; OTHER INFORMATION: P-CMV 35S
; NAME/KEY: CDS
; LOCATION: (526)..(1320)
; OTHER INFORMATION: npfII
; NAME/KEY: transcription termination & polyadenylation sequence
; LOCATION: (1325)..(1767)
; OTHER INFORMATION: T-AGRTu.nos3'
; NAME/KEY: promoter
; LOCATION: (1809)..(2386)
; OTHER INFORMATION: P-FMV
; NAME/KEY: 5'UTR
; LOCATION: (2407)..(2480)
; OTHER INFORMATION: L-Os.betabub
; NAME/KEY: Intron
; LOCATION: (2498)..(2614)
; OTHER INFORMATION: I-Os.PAL
; NAME/KEY: transit_peptide
; LOCATION: (2644)..(2790)
; OTHER INFORMATION: TP-Zm.rbcS
; NAME/KEY: Intron
; LOCATION: (2791)..(2953)
; OTHER INFORMATION: I-Zm.rbcS
; NAME/KEY: transit_peptide
; LOCATION: (2954)..(3040)
; OTHER INFORMATION: TP-Zm.rbcS
; NAME/KEY: CDS
; LOCATION: (3041)..(6730)
; OTHER INFORMATION: CryIbB variant
; NAME/KEY: transcription termination sequence
; LOCATION: (6731)..(6736)
; OTHER INFORMATION: miscellaneous sequence
; NAME/KEY: polyadenylation sequence
; LOCATION: (6742)..(6981)
; OTHER INFORMATION: T-Os.LDH
US-10-525-318-8

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Query Match 38.0%; Score 279.6; DB 6; Length 7000;
Best Local Similarity 98.3%; Pred. No. 1.6e-82;
Matches 293; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 437 CTATCTGTCACTTCAATCAAAAGGACAGTGAAGAGGAGTGCACCTACAAATGCCATC 496
DB 174 CTATCTGTCACTTCAATCAAAAGGACAGTGAAGAGGAGTGCACCTACAAATGCCATC 233

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OY 497 ATTCGATTAAGAAAGGCTATCTTCAGATGCTCTGCGACAGTGTGCTCCAAAGATG 556  
DB 234 ATTCGATTAAGAAAGGCTATCTTCAGATGCTCTGCGACAGTGTGCTCCAAAGATG 293  
OY 557 GACCCCAACCCAG 616  
DB 294 GACCCCAACCCAG 353  
OY 617 AAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 675  
DB 354 AAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413  
OY 676 TCCGAGAGCCCTTCTCTCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 733  
DB 414 TCCGAGAGCCCTTCTCTCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 471

## RESULT 9

US-11-248-986-31  
Sequence 31, Application US/11248986  
Publication No. US20060112448A1  
GENERAL INFORMATION:  
APPLICANT: OSBOURN, ANNE E.  
APPLICANT: OI, XIAOQUAN  
TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS  
FILE REFERENCE: BBI550 US NA  
CURRENT APPLICATION NUMBER: US/11/248,986  
PRIORITY DATE: 2005-10-12  
PRIORITY APPLICATION NUMBER: 60/619,203  
PRIORITY FILING DATE: 2004-10-15  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 31  
LENGTH: 2574  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Soybean recombinant DNA construct 1  
US-11-248-986-31

Query Match 34.4%, Score 253.4, DB 7, Length 2574,  
Base Local Similarity 99.6%, Pctd No 4, e-74,  
Matches 254, Conservative 0, Mismatches 1, Indels 0, Gaps 0,  
OY 121 AGTGAAGCTTTTCACAAAGGATTAATCGGAAAGCTCTCGGATTCATGCGCAGCT 180  
DB 222 ATGTAAGCTTTTCACAAAGGATTAATCGGAAAGCTCTCGGATTCATGCGCAGCT 281  
OY 181 ATCTGCTCTTCATCAAAAGCAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
DB 282 ATCTGCTCTTCATCAAAAGCAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 341  
OY 241 TCCGATTAAGAAAGGCTATCTTCAGATGCTCTGCGACAGTGTGCTCCAAAGATG 300  
DB 342 ATTCGATTAAGAAAGGCTATCTTCAGATGCTCTGCGACAGTGTGCTCCAAAGATG 401  
OY 301 CCCCACCCAG 360  
DB 402 CCCCACCCAG 461  
OY 361 GTGATGATGATGAT 375  
DB 462 GTGATGATGATGAT 476

RESULT 10  
US-11-248-986-32  
Sequence 32, Application US/11248986  
Publication No. US20060112448A1  
GENERAL INFORMATION:  
APPLICANT: OSBOURN, ANNE E.  
APPLICANT: OI, XIAOQUAN

TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS  
FILE REFERENCE: BBI550 US NA  
CURRENT APPLICATION NUMBER: US/11/248,986  
PRIORITY DATE: 2005-10-12  
PRIORITY APPLICATION NUMBER: 60/619,203  
PRIORITY FILING DATE: 2004-10-15  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 32  
LENGTH: 6889  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Soybean Recombinant DNA construct 2  
US-11-248-986-32

Query Match 34.4%, Score 253.4, DB 7, Length 6889,  
Base Local Similarity 99.6%, Pctd No 4, e-74,  
Matches 254, Conservative 0, Mismatches 1, Indels 0, Gaps 0,  
OY 121 AGTGAAGCTTTTCACAAAGGATTAATCGGAAAGCTCTCGGATTCATGCGCAGCT 180  
DB 222 ATGTAAGCTTTTCACAAAGGATTAATCGGAAAGCTCTCGGATTCATGCGCAGCT 281  
OY 181 ATCTGCTCTTCATCAAAAGCAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
DB 282 ATCTGCTCTTCATCAAAAGCAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 341  
OY 241 TCCGATTAAGAAAGGCTATCTTCAGATGCTCTGCGACAGTGTGCTCCAAAGATG 300  
DB 342 ATTCGATTAAGAAAGGCTATCTTCAGATGCTCTGCGACAGTGTGCTCCAAAGATG 401  
OY 301 CCCCACCCAG 360  
DB 402 CCCCACCCAG 461  
OY 361 GTGATGATGATGAT 375  
DB 462 GTGATGATGATGAT 476

## RESULT 11

US-10-523-290-7/c  
Sequence 7, Application US/10523290  
Publication No. US20060095986A1  
GENERAL INFORMATION:  
APPLICANT: Johnson, Scott C.  
APPLICANT: Cavato, Tracey R.  
TITLE OF INVENTION: CORN EVENT PV-ZMIR13 (MON863) PLANTS AND COMPOSITIONS AND METHOD  
FILE REFERENCE: 38-21 (52221)B  
CURRENT APPLICATION NUMBER: US/10/523,290  
PRIORITY DATE: 2003-07-29  
PRIORITY APPLICATION NUMBER: 60/399,279  
PRIORITY FILING DATE: 2002-07-29  
PRIORITY APPLICATION NUMBER: PCT/US03/22860  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 266  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 5' insert sequence  
NAME/KEY: DNA  
LOCATION: (1)...(266)  
OTHER INFORMATION: 5' insert sequence  
US-10-523-290-7

Query Match 32.9%, Score 242, DB 6, Length 266,  
Base Local Similarity 99.6%, Pctd No 4, e-74,  
Matches 254, Conservative 0, Mismatches 1, Indels 0, Gaps 0,  
OY 121 AGTGAAGCTTTTCACAAAGGATTAATCGGAAAGCTCTCGGATTCATGCGCAGCT 180  
DB 222 ATGTAAGCTTTTCACAAAGGATTAATCGGAAAGCTCTCGGATTCATGCGCAGCT 281  
OY 181 ATCTGCTCTTCATCAAAAGCAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
DB 282 ATCTGCTCTTCATCAAAAGCAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 341  
OY 241 TCCGATTAAGAAAGGCTATCTTCAGATGCTCTGCGACAGTGTGCTCCAAAGATG 300  
DB 342 ATTCGATTAAGAAAGGCTATCTTCAGATGCTCTGCGACAGTGTGCTCCAAAGATG 401  
OY 301 CCCCACCCAG 360  
DB 402 CCCCACCCAG 461  
OY 361 GTGATGATGATGAT 375  
DB 462 GTGATGATGATGAT 476

Best Local Similarity 96.1%; Pred. No. 7.9e-71;  
Matches 248; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 427 CATTGCCAGCTATCTGTCTCACTTCATCAAAAGGACAGTAGAAAAGGAGTGGCACTTAC 486  
DB |||||  
QY 487 AAATGCCATCATTCGGATTAAGGAAAGGCTATCTCTCAAGATCTCTCTGCGACATGGT 546  
DB |||||  
QY 547 CCCAAAGATGGACCCGCCACGAGGAGCATCTGTGAAAAAGAGAGCTTCCAAACACG 606  
DB |||||  
QY 607 TCTTCAAGCAAGTGGATGTATCTCCATGCTAGCTTAAGGATGAACCAATCC 666  
DB |||||  
QY 667 CACTATCTCTCGCAAGAC 684  
DB |||||

## RESULT 12

US-10-523-290-3/c  
; Sequence 3, Application US/10523290  
; Publication No. US2006005986A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Scott C.  
; APPLICANT: Corallo, Timothy R.  
; TITLE OF INVENTION: CORN EVENT PV-2MR13 (MON863) PLANTS AND COMPOSITIONS AND METHODS THEREOF  
; FILE REFERENCE: 38-21 (52221)B  
; CURRENT APPLICATION NUMBER: US/10/523,290  
; PRIOR FILING DATE: 2005-02-03  
; PRIOR APPLICATION NUMBER: PCT/US03/22860  
; PRIOR FILING DATE: 2003-07-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 508  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5' genome + insert sequence  
; NAME/KEY: DNA  
; LOCATION: (1)..(508)  
; OTHER INFORMATION: 5' genome + insert sequence  
US-10-523-290-3

Query Match  
Best Local Similarity 96.1%; Pred. No. 1.1e-6;  
Matches 248; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 427 CATTGCCAGCTATCTGTCTCACTTCATCAAAAGGACAGTAGAAAAGGAGTGGCACTTAC 486  
DB |||||  
QY 487 AAATGCCATCATTCGGATTAAGGAAAGGCTATCTCTCAAGATCTCTCTGCGACATGGT 546  
DB |||||  
QY 547 CCCAAAGATGGACCCGCCACGAGGAGCATCTGTGAAAAAGAGAGCTTCCAAACACG 606  
DB |||||  
QY 607 TCTTCAAGCAAGTGGATGTATCTCCATGCTAGCTTAAGGATGAACCAATCC 666  
DB |||||

DB 78 TCTTCAAGCAAGTGGATGTATCTCTCACTGATGATCGTAGGAGTGGCAATCC 19  
QY 667 CACTATCTCTCGCAAGAC 684  
DB |||||  
DB 18 CACTATCTCTCGCAAGAC 1

## RESULT 13

US-10-525-318-11/c  
; Sequence 13, Application US/10525318  
; Publication No. US20060112447A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; APPLICANT: Bogdanova, Natalia N  
; TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expression  
; FILE REFERENCE: 38-21 (15414)  
; CURRENT APPLICATION NUMBER: US/10/525,318  
; PRIOR FILING DATE: 2005-02-23  
; PRIOR APPLICATION NUMBER: 60/407,428  
; PRIOR FILING DATE: 2004-08-29  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 5170  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fully synthetic expression cassette  
; NAME/KEY: promoter  
; LOCATION: (26)..(640)  
; OTHER INFORMATION: P-e35S  
; NAME/KEY: 5'UTR  
; LOCATION: (665)..(735)  
; OTHER INFORMATION: L-Ta.CAB  
; NAME/KEY: Intron  
; LOCATION: (749)..(1239)  
; OTHER INFORMATION: 1-Oe.ACT1  
; NAME/KEY: CDS  
; LOCATION: (1241)..(4930)  
; OTHER INFORMATION: Cry1Bb variant  
; NAME/KEY: transcription termination sequence  
; LOCATION: (4931)..(4936)  
; OTHER INFORMATION: miscellaneous  
; NAME/KEY: polyadenylation sequence  
; LOCATION: (4937)..(5170)  
; OTHER INFORMATION: T-Ta.hsp70  
US-10-525-318-11

Query Match  
Best Local Similarity 13.5%; Score 99.2; DB 6; Length 5170;  
Matches 101; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CAGCGTGCTCTCTCCAAATGAATGAATCTCTTATATAGAGAGAGGCTCTTCCGAGCA 65  
DB 647 CAGCGTGCTCTCTCCAAATGAATGAATCTCTTATATAGAGAGAGGCTCTTCCGAGCA 588  
QY 66 TAGTGGGATGTGCGTCATCCCTTACGTGAGGATGATCTGCA 109  
DB 587 TAGTGGGATGTGCGTCATCCCTTACGTGAGGATGATCTGCA 544

RESULT 14  
US-10-525-318-11/c  
; Sequence 13, Application US/10525318  
; Publication No. US20060112447A1

GENERAL INFORMATION:  
APPLICANT: Monsanto Technology LLC  
APPLICANT: Romano, Charles P  
APPLICANT: Bogdanova, Natalie N  
TITLE OF INVENTION: Nucleotide Sequences Encoding CryIb Proteins for Enhanced Expression  
FILE REFERENCE: 38-21(15414)  
CURRENT APPLICATION NUMBER: US/10/525,318  
PRIORITY DATE: 2005-12-23  
PRIORITY APPLICATION NUMBER: 60/607,428  
PRIORITY FILING DATE: 2002-08-25  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 13  
LENGTH: 5600  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: Promoter  
LOCATION: (126)..(1640)  
OTHER INFORMATION: P-6355  
FEATURE:  
NAME/KEY: 5' UTR  
LOCATION: (665)..(735)  
OTHER INFORMATION: L-Ta, CAB  
FEATURE:  
NAME/KEY: Intron  
LOCATION: (749)..(1239)  
OTHER INFORMATION: I-08:ACT1  
FEATURE:  
NAME/KEY: Transic peptide  
LOCATION: (1255)..(1401)  
OTHER INFORMATION: TP-Zm, rbcS  
FEATURE:  
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LOCATION: (1402)..(1564)  
OTHER INFORMATION: I-Zm, rbcS  
FEATURE:  
NAME/KEY: Transic peptide  
LOCATION: (1565)..(1651)  
OTHER INFORMATION: TP-Zm, rbcS  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1652)..(5341)  
OTHER INFORMATION: CryIb variant  
FEATURE:  
NAME/KEY: Transcription termination sequence  
LOCATION: (5342)..(5347)  
OTHER INFORMATION: miscellaneous  
FEATURE:  
NAME/KEY: Polyadenylation sequence  
LOCATION: (5350)..(5592)  
OTHER INFORMATION: T-08, LDR  
US-10-525-318-13

Query Match 13.5% Score 99.2; DB 6; Length 5600;  
Best Local Similarity 97.1%; Pred. No. 5e-23; 3; Indels 0; Gaps 0;  
Matches 101; Conservative 0; Mismatches 0;

QY 6 CAGGCTGCTCTCCCAATGAATGAATCTCTTATATAGAGAGAGGCTCTTGCGAAGA 65  
DB 647 CAGGCTGCTCTCTCCCAATGAATGAATGAATCTCTTATATAGAGAGAGGCTCTTGCGAAGA 588  
QY 66 TAGTGGAATGTCCTCTCAATCTCTTATAGTCACTGCAAGACTGCA 109  
DB 587 TAGTGGAATGTCCTCTCAATCTCTTATAGTCACTGCAAGACTGCA 544

RESULT 15  
US-11-258-704-40  
Sequence 40, Application US/11258704

Publication No. US20060101545A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Zhan-Bin  
APPLICANT: Stoop, Johan  
TITLE OF INVENTION: PW2 AND LEA3 PROMOTERS AND USE IN EXPRESSION OF TRANSGENIC GEN  
FILE REFERENCE: 88-1551  
CURRENT APPLICATION NUMBER: US/11/258,704  
PRIORITY DATE: 2005-12-23  
PRIORITY APPLICATION NUMBER: US/60/625,835  
PRIORITY FILING DATE: 2004-11-08  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 40  
LENGTH: 8810  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
NAME/KEY: plasmid SH50  
US-11-258-704-40

Query Match 13.4% Score 98.8; DB 7; Length 8810;  
Best Local Similarity 98.0%; Pred. No. 8.5e-23;  
Matches 100; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GATCCAGCGTCTCTCTCCCAATGAATGAATCTCTTATATAGAGAGAGGCTCTTGCGA 61  
DB 3854 GCTCGAGCGTCTCTCTCCCAATGAATGAATCTCTTATATAGAGAGAGGCTCTTGCGA 3913  
QY 62 AGAATAGCGATTTGGCTCATCTCTTACCTGATGAGACT 103  
DB 3914 AGAATAGCGATTTGGCTCATCTCTTACCTGATGAGACT 3955

Search completed: June 5, 2006, 06:01:22  
Job time : 30 secs



from the midpoint of the main stem.  
/dev. stage=Vascular cambium, and bark  
from trees harvested 1 and 7 days after girdling  
treatment.  
/lab. host= *P. colli* DB10b cells  
/cell. line= GQ00b: Cambium, phloem and bark of girdled  
saplings.  
/note=Approximately 60 cm tall; Vector: plasmidectric II SR (+)  
XR. Site 1: Eco-RI; Site 2: Xho-1; Tissues were pooled  
from above and below the girdle. cDNA was prepared from  
mg of poly A+ selected RNA and was directionally ligated  
into the plasmidectric II SR (+) XR vector (Stratagene),  
transformed by electroporation into DB10b cells (in  
lignum) for propagation.

**ORIGIN**

	Query Match	74.3%	Score 546.6	DB 5	Length 698
	Best Local Similarity	94.7%	Pred. No. 2.7e-169		
	Matches 577	Conservative 0	Mismatches 29	Indels 3	Gaps 1
QY	121	AGTGAACCTTTCAACAAAGGATATATCGGAAAACCTCTCGGAAATTCATTGCTCCAGCT	180		
DB	4	ATTGAGACCTTTCAACAAAGGATATATCGGAAAACCTCTCGGAAATTCATTGCTCCAGCT	63		
QY	181	ATTGGAATCTTCAACAAAGGATATATCGGAAAACCTCTCGGAAATTCATTGCTCCAGCT	240		
DB	64	ATTCTCTCACTTATATGTGAAGATATGTGAAAAGGATGCTGCTCTTCAAAATTCCTCAT	123		
QY	241	TGCGATTAAGAAAGGCTATTCCTTCAGAAATCCTCTGCGCAAGATGGTCCCAAGATGGA	300		
DB	124	TTCGATTAAGAAAGGCTATTCCTTCAGAAATCCTCTGCGCAAGATGGTCCCAAGATGGA	183		
QY	301	CCCCACCCACGAGAGAGATCTGTGAAAAGAAAGATTCACACCAAGCTTCAAGCA	360		
DB	184	CCCCACCCACGAGAGAGATCTGTGAAAAGAAAGATTCACACCAAGCTTCAAGCA	243		
QY	361	GTGGAATTAATGTAATTTG---CACTGAACCTTTCAACAAAGGATATTCGGAACCTC	417		
DB	244	GTGAATTAATGTAATTTGCTCCGATTAATGATCTTTCAACAAAGGATATTCGGAACCTC	303		
QY	418	CTTGGATTCGAATTTGGCCAGAGCTATCTGTGCTCTTCAAAAGGACGTAAAGAAAGAT	477		
DB	304	CTTGGATTCGAATTTGGCCAGAGCTATCTGTGCTCTTATTTGTGAAGATATGTGAAAAGGAAAGT	363		
QY	478	GGCAGCTCAAGAAATGCCACATATGCGATAAAGGAAAGGCTATGCTTCAAGATGCTCTGCC	537		
DB	364	GGCTCTCAAGAAATGCCACATATGCGATAAAGGAAAGGCTATGCTTCAAGATGCTCTGCC	423		
QY	538	GACATGTGTTCCCAAGATGAGACCCCAACCCCAAGAGACATGTGTGAAAAGAAAGAT	597		
DB	424	GACATGTGTTCCCAAGATGAGACCCCAACCCCAAGAGACATGTGTGAAAAGAAAGAT	483		
QY	598	GCATACACCTGCTTCAAGACAGTGAATTTGAATGTGATATTCATCATCTTAAGAGATAC	657		
DB	484	GCATACACCTGCTTCAAGACAGTGAATTTGAATGTGATATTCATCATCTTAAGAGATAC	543		
QY	658	GCACATATCCCATATCTTGTGGAAAGACCCCTGCTCATATTAAGAAATTCATTCAATTTG	717		
DB	544	GCACATATCCCATATCTTGTGGAAAGACCCCTGCTCATATTAAGAAATTCATTCAATTTG	603		
QY	718	GAGAGAGACA	726		
DB	604	GAGAGAGACA	612		

RESULT 2	
COA72768	
LOCUS	COA72768
DEFINITION	GQ0061.BR.1.K09 GQ006: Camblum, phloem and bark of glided haplings
	Picea glauca cDNA clone GenomeQuebec_Id:GQ0061K09 5', mRNA
	sequence.
ACCESSION	COA72768

VERSION	COA72766.1	GI:50141325
KEYWORDS	EST	
SOURCE	Picea glauca (white spruce)	
ORGANISM	Picea glauca (Pinellales, Streptophyta; Embryophyta; Tracheophyta)	
REFERENCE	Spencer, D.P., Conteropoulou, C., Conterlas, P., Pinaceae, Picea	
AUTHORS	1 (bases 1 to 702)	
TITLE	Moravcsy, M., J., Cooke, J., Pav, N., Parsons, L., Paul, C., Seguin, A.,	
JOURNAL	Recey, B., Butterfield, Y., Barberis, S., Yang, G., Scott, J.,	
COMMENT	Siddiqui, A., Holt, R., Marz, M., and Mackay, J.	
	Arabidopsis EST sequencing in Picea glauca (white spruce)	
	Unpublished (2004)	
	Contact: John Mackay	
	Department of Biology, University of Alberta	

**COMMENT**

Pavillon Charles-Émile Marchand, Québec, Canada QK 7P4  
 Fax: 418 556 7493  
 Email: jmackey@vsu.ulaval.ca  
 Center for Computational Genomics and Bioinformatics (CCGB),  
 University of Minnesota, MN id Identifier: MNS197113 Clone ID:  
 G00081.BK K09 Clones available through: John Mackay, Ph. D.  
 Professeur adjoint - Assistant professeur EMAIL:  
 jmackey@vsu.ulaval.ca Centre de Recherche en Biologie Forestière  
 (Forest Biology Research Center) Université Laval Québec, Québec  
 Canada QK 7P4  
 Place: 1.BR row: 03 column: K  
 Seq primer: M13 Reverse Primer.

## FEATURES

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/retain_pg="533"
/clone_id="11310"
/clone_name="Quebec"
/sex="Hemaphrodite"
/issue_type="Vascular cambium, secondary phloem and bark
of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/new_stage="Vascular cambium, secondary phloem, and bark
treatment harvested 1 and 7 days after girdling"
/lab_host="E. coli DH10B cells"
/clone_idb="QG008: Cambium, phloem and bark of girdled
saplings"
/note="Organ: Main stem of 4 year old saplings,
approximately 60 cm tall. Vector: phloemscript II SK (+)
X1; Site: 1 and 2; Age: 4; Sex: female; Media: 666 mg
of poly A selected RNA and was directionally ligated
into the phloemscript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (in
vitro) for propagation"

```

ORIGIN

	Query Match	Best Local Similarity	74.3%	Score 546.6, DB 8	Length 702	
	Matches 577	Conservative 0	Pred. No. 2.76-160	Mismatches 29	Indels 3	Gaps 1
Oy	121	AGTGGAGCTTTTCACAAAGGGGTATATTCGGGAAACCTCTCGGATATTCATATGCCCAAGT	180			
Db	29	ATTGGAGCTTTTCACAAAGGGATATATTCGGGAAACCTCTCGGATATTCATATGCCCAAGT	180			
Oy	181	ATCTGTCACTTCACTCAAAAGACAGTGTGAAGAAAGGATGTGTGCATCTCAATATGGCCATCT	240			
Db	89	ATGTGTCACTTCACTCAAAAGATGTGTGAAGAAAGGATGTGTGCATCTCTTCAAAATGTGCATCT	148			
Oy	241	TGCGATAAAGAAAGGCTCATGTGTCAAGATGTGCTCTGTGCGACACAGTGTGTCCCAAGATGGA	300			
Db	149	TGCGATAAAGAAAGGCTCATGTGTCAAGATGTGCTCTGTGCGACAGTGTGTCCCAAGATGGA	208			
Oy	301	CCCCCAACCCACAGACGATGTGTGAAGAAAGAAAGCAAGTTTCCACACAGTCTTCAAGACAA	360			
Db	209	CCCCCAACCCACAGACGATGTGTGAAGAAAGAAAGCAAGTTTCCACACAGTCTTCAAGACAA	268			



VERSION	KEYWORDS	COA72761.1	GI:50141306
SOURCE	ORGANISM	Picea glauca (white spruce)	
REFERENCE	AUTHORS	Bukacinski, V.; Vidilaplanee, S.; Streptophyta; Embryophyta; Tracheophyta; Equisetophyta; Lycopodiophyta; Charadeles; Pinaceae; Piceae.	
TITLE	JOURNAL	Morency, M., J. Cooke, J., Ray, N., Parsons, L., Paul, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stettin, J., Siddiqui, A., Holt, R., Marx, M., and Mackay, J.	
COMMENT		Arbores EST sequencing in Picea glauca (white spruce) Unpublished (2004) Contact: John Mackay Centre de Recherche en Biologie Forestiere Universite Laval Pavillon Charles-Émile Bouchard, Quebec, CANADA G1K 7P4 Fax: 418 656 7493 E-mail: john.mackay@biologie.ulaval.ca Center for Computational Genomics and Bioinformatics (CCGB) University of Minnesota, MN ID Identifier: MN5198052 Clone ID: GQ0001.BR.907 Clones available through: John Mackay, Ph. D. Professeur adjoint, Assistant professor EMAIL: j.mackay@ccgb.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA G1K 7P4 Plate: 1.BR. row: 07 column: G Seq primer: M13 Reverse primer. Location/Qualities 1000 803 /organism="Picea glauca" /mol_type="mRNA" /db_xref="taxon:3330" /db_xref="Pgi:653" /clone="GenomeQuebec_ID:GQ0001907" /sex="hemaphrodite" /tissue_type="Vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main secondary phloem, and bark from trees harvested 1 and 7 days after girdling treatment" /lib_host="P. coll DHIO cells" /clone_lib="GQ0008: Cambium, phloem and bark of girdled saplings" /note="Organ: Main stem of 4 year old saplings, approximately 60 cm tall; Vector: plasmidscript II SK (+) XR, Site:1; Eco-RI; Site:2; Xho-I; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the BamHI-XhoI SK(+) XhoI (pGissegren) transformed by electroporation into DHIO cells (in vitro) for propagation"	
ORIGIN			
Query Match		74.3%; Score 546.6; DB 8; Length 803;	
Best Local Similarity		94.7%; Pred. No. 2,86-160;	
Matches 577;		Conservative 0; Mismatches 29; Indels 3; Gaps 1.	
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Db	31	ATTGAAAGATTTCACAAAGCGAGTAATATCGGAAAGCTCTCGGATTCATCTGCCAGCT	90
Db	181	ATCTGTCATCTCAACAAAGGACGATGAAGAAAGAGGACACCTCCAAATGCGATCAT	240
Db	91	ATCTGTCATCTTAATGGAAGATATGCGAAAGGAGGCTCTCCAAATGCGATCAT	150
Db	241	TGCGATAAAGAAAGGCTATGCTTCAACATGCTCTCCGACAGTGGTCCAAAGATGGA	300
Db	151	TGCGATAAAGAAAGGCTATGCGTAAGAAAGGAGGCTCTCCGACAGTGGTCCAAAGATGGA	210
Db	301	CGCCGACCCCAAGAGGCTATGCGTAAGAAAGGAGGCTCTCCGACAGTGGTCCAAAGATGGA	360
Db	211	CGCCGACCCCAAGAGGCTATGCGTAAGAAAGGAGGCTCTCCGACAGTGGTCCAAAGATGGA	270

Oy		361	GCGAGATTTGATTGTATGG---CACTGAACACTTTCCTCCAAACAAGGGTAATAATTCGGAAAACCTC	417
Dy		271	TGGATATATATATCATGCTGCATTCAGAACATTTTCCTCAAACAAAGAGATTAATTCGGAAAACCTC	330
Oy		418	CCTGGAGATCTATGGCCAGCTATCTTGCTATCTTCCTCAAAGAAGATGAATAGAAAAAGAGCT	479
Dy		331	CTCGAATCTCATTTGCCAGCTATCTGCTCATTTATTGTGAAGATATGAGAAAAAGAAAGCT	390
Oy		478	GGCACCTTAACAAMTAGCCATCATTTGGAGTAAAGAAAGAGCTTCTGTCCTCAAGAGCTCTGCC	537
Dy		331	GGCTCTCAACAAGATGCCATCATTTGGAGTAAAGAAAGAGCTCTGTCCTCAAGAGCTCTGCC	450
Oy		511	CCAAACACTCTCTCAACAAAGAGATTATGATGATATCTCCACCTGACCTAAAGGATATAC	570
Oy		658	GCACATCCCATCTATCTCTCCAGAAACCCTCTCTCATATTAAGAAATCTTCAATTTG	717
Dy		571	GACACATCCCATCTATCTCTCCAGAAACCCTCTCTCATATTAAGAAATCTTCAATTTG	630
Oy		718	GAGAGACG	726
Dy		631	GAGAGACG	639
RESULT 5				
DOCS	CK437984		713 bp.	mRNA linear EST 08-JAN-2000
DEFINITION	GM0001 BP K09 GM0008 Cambium phloem and bark of girdled saplings			
ACCESSION	Picea glauca cDNA clone GQ0001_K09 5'			mRNA sequence.
VERSION	CK437984			
KEYWORDS	EST.			
SOURCE	Picea glauca (white spruce)			
ORGANISM	Bakaeyer; Vitrifidplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Coniferopsida; Conitretidae; Pinaceae; Picea. Morency M.-J Cooke J., Parvy N., Patenaon L., Pale C., Seguin A., Rezeau E., Butterfield Y., Barber S., Yang-G, Stett J., Sidiqui A., Holt R., Marz M. and Mackay J. Arbores EST sequencing in Picea glauca (white spruce) Unpublished (2004) Contacte : John MacKay Centre de Recherche en Biologie Forestiere Universite Laval Rayillon Charles-Eugene Marchand, Quebec, Canada G1K 7P4 Email : jmackays@vs.laval.ca Center for Computational Genomics and Bioinformatics (CCGB), University of Minnesota, MN id Identifier: KM517386 Clons ID: GQ0001_K09 Clones available Througjh: John Mackay, Ph.D. Professeur adjoint -Assistant professor EMAIL: jmackays@vs.laval.ca Centre de Recherche en Biologie Forestiere [Forest Biology Research Center] Universite Laval Quebec, Quebec CANADA G1K 7P4 Plate: 1 row, 09 columns: K Seq primer(s) Location/Qualifiers			
TITLE	GENE			
COMMENT				
FEATURES				
source	/organism='Picea glauca' /mol_type='mRNA' /strain='Pg-653' /db_xref='taxon:3330' /clone='GQ0001_K09' /near_Hemaphysaloides' from the midpoot by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem"			







**ORGANISM** Picea glauca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Coniferopsida; Pinaceae; Picea.

**REFERENCE** 1 (bases 1 to 736)

**AUTHORS** Morency, M.-J., Cooke, J., Pavly, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Scott, J., Siddiqui, A., Holt, R., Marra, M., and Mackay, J.

**TITLE** Arborea EST sequencing in Picea glauca (white spruce)

**JOURNAL** Unpublished (2004)

**COMMENT** Contact: John Mackay  
Centre de Recherche en Biologie Forestiere  
Universite Laval Quebec, Quebec, Canada G1K 7P4  
Pavillon Charles-Eugene Marchand,  
Fax: 418 656 7493  
Email: jmackay@svs.ulaval.ca  
Center for Computational Genomics and Bioinformatics (CCGB),  
University of Minnesota, MN id Identifier: MN5174611 Clone ID:  
GQ0085\_M24 Clones available through: John Mackay, Ph. D. Professeur  
adjoint - Assistant professor EMAIL: jmackay@svs.ulaval.ca Centre  
de Recherche en Biologie Forestiere (Forest Biology Research  
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4  
Seq primer: M3 Reverse Primer.  
Size: 5' row: 24 column: W  
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of trees girdled by removing a ring of bark ca. 1 cm wide  
from the midpoint of the main stem"  
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from trees harvested 1 and 7 days after girdling  
treatment"  
/lab\_hosts="E. coli DH10B cells"  
/accession="GQ0085\_M24"  
/note="Organ: Main stem of 4 year old saplings,  
approximately 60 cm tall; Vector: pBluescript II SK (+)  
XR; Site 1: Eco-R; Site 2: Xho-I; Tissues were pooled  
from above and below the girdle. cDNA was prepared from 5  
mg of poly A+ selected RNA and was directionally ligated  
into the pBluescript II SK (+) XR vector (Stratagene),  
transformed by electroporation into DH10B cells (In  
vitrogen) for propagation"

**ORIGIN**

Query Match 72.7%; Score 535.2; DB 5; Length 736;  
Best Local Similarity 94.8%; Prot No. 156;  
Matches 565; Conservative

QY 121 AGTGAGACTTTTCAACAAAGGGATATATCGGAACCTCTCGGATTCATTGSCCAGCT 180  
Db 40 ATTGAGACTTTTCAACAAAGGGATATATCGGAACCTCTCGGATTCATTGSCCAGCT 99

QY 181 ATCTGTCACTTCATCAAAAAGGACAGTAGAAGAAGGTGGCACTTAACAATGCCCATCAT 240  
Db 100 ATCTGTCACTTCATTCATTCAGAGATATGCGAAGAAGGTGGCTTCTCAAAATGCCCATCAT 159

QY 241 TGCGATTAAGAGAGAGATTCGTTGAGATGCCTCTTCGCAAGTGTGCTCCCAAGATGGA 300  
Db 160 TGCGATTAAGAGAGAGATTCGTTGAGATGCCTCTTCGCAAGTGTGCTCCCAAGATGGA 219

QY 301 CCCCCACCACGAGGAGCATGTTGGAAGAAGAGAGAGTTCACACGCTCTCAAGATGGA 360  
Db 220 CCCCCACCACGAGGAGCATGTTGGAAGAAGAGAGAGTTCACACGCTCTCAAGATGGA 279

QY 361 GTGGATTATGTGATTG-- --CAGTGAGACTTTTTCAACAAGGGTATATTCGGGAACCTC 417  
Db 280 GTGGATTATGTGATTGTCCTCAATTCGATCTTTTCAACAAGGGTATATTCGGGAACCTC 339

approximately 60 cm tall; Vector: pBluescript II SK (+)  
 XR; Site 1: Eco-RI; Site 2: Xho-I; Tissues were pooled  
 from above and below the gland. cDNA was prepared from 5  
 mg of poly A+ selected RNA and was directionally ligated  
 into the pBluescript II SK (+) XR vector (Stratagene),  
 transformed by electroporation into DH10B cells (in  
 vitro) for propagation."

Query Match 72.4%; Score 533.2; DB 5; Length 698;  
 Best Local Similarity 94.5%; Pred. No. 4,4e-156;  
 Matches 563; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

ORIGIN

```

OY 121 AGTGAAGATTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATGCGCAAGCT 180
DB 37 ATGTGAGATTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATGCGCAAGCT 96
OY 181 ATGTGATCTTCATCAAAAGACAGTGAAGAGAGAGTGCACCTTACAAATGTCATCT 240
DB 97 ATGTGATCTTCATTCATGAGATAGTGAAGAGAGAGTGCATCTTACAAATGTCATCT 186
OY 241 TGGCAATTAAGAAAGGCTATGCTTCAAGATGCTCTCGGACAGTGGTCCCAAGATGGA 300
DB 157 TGGCAATTAAGAAAGGCTATGCTTCAAGATGCTCTCGGACAGTGGTCCCAAGATGGA 216
OY 301 CCCCAACCAAGAGAGCATCTGGAAGAAAGAGAGTTCACACAGCTCTTCAAGAGCA 360
DB 217 CCCCAACCAAGAGAGCATCTGGAAGAAAGAGAGTTCACACAGCTCTTCAAGAGCA 276
OY 361 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417
DB 277 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 336
OY 418 CTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
DB 337 CTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 396
OY 478 GGCACCTCTCAAAATGCTATGCTGATGATGATGATGATGATGATGATGATGATGATG 537
DB 397 GGCCTCTCAAAATGCTATGCTGATGATGATGATGATGATGATGATGATGATGATG 456
OY 538 GACAGTGTCCCAAGATGACCCCAACCAAGAGAGATGCTGGAAGAAAGAGCTT 597
DB 457 GACAGTGTCCCAAGATGACCCCAACCAAGAGAGATGCTGGAAGAAAGAGCTT 516
OY 598 GCACCAAGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 657
DB 517 GCACCAAGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 576
OY 658 GCACCAATGCTATGCTGCAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 713
DB 577 GCACCAATGCTATGCTGCAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 632

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RESULT 10  
 CD481168 610 bp mRNA linear EST 29-JUN-2005  
 LOCUS GQ0165.B7 M24 G0016: Primary, secondary SHOOT -N fertill. Tissue  
 DEFINITION Picea glauca cDNA clone GenomeQuebec\_id:GQ0165M24.3, mRNA  
 sequence.  
 ACCESSION CO481168  
 VERSION CO481168.1 GI:50160512  
 KEYWORDS EST.  
 SOURCE Picea glauca (white spruce)  
 ORGANISM Picea glauca  
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
 REFERENCES  
 AUTHORS Morehouse, J., Cooke, J., Pay, N., Parsons, L., Pail, C., Seglin, A.,  
 Ressel, F., Butterfield, Y., Barber, S., Yang, G., Stett, R.,  
 Siddiqui, A., Holt, R., Werra, M. and Mackay, J.  
 TITLE Arborea EST sequencing in Picea glauca (white spruce)  
 JOURNAL Unpublished (2004)

## COMMENT

Contact: John Mackay  
 Centre de Recherche en Biologie Forestiere  
 Universite Laval  
 Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4  
 Fax: 418 656 7493  
 Email: jmackay@rsb.ulaval.ca  
 Center for Computational Genomics and Bioinformatics (CCGB),  
 University of Minnesota, MN, ID Identifier: 1026954 (Comp ID,  
 01/05/2005) (http://www.ccg.umn.edu/~jcmackay/)  
 adjoint "Assistant professeur EMILU" jmackay@rsb.ulaval.ca Centre  
 de Recherche en Biologie Forestiere (Forest Biology Research  
 Center) Universite Laval Quebec, Quebec CANADA G1K 7P4  
 Plates: 5 row: 24 column: M  
 Seq primer: T7 Primer.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /seq\_id="GQ0165M24"  
 /seq="Hermaphrodite"  
 /tissue\_type="xylem, pith, cambium, phloem, bark"  
 /dev\_stage="Primary & secondary shoot, secondary phloem  
 pooled from plants fertilized with low and high NH4NO3"  
 /lab\_host="E. coli DH10B cells"  
 /clone\_id="GQ016: Primary, secondary SHOOT -N fertill.  
 Tissue"  
 /note="Organ: Main stem region producing secondary growth  
 on 60 cm tall seedlings; Vector: pBluescript II SK (+) XR;  
 Site 1: Eco-RI; Site 2: Xho-I; cDNA was prepared from 5 mg  
 of poly A+ selected RNA and was directionally ligated into  
 the pBluescript II SK (+) XR vector (Stratagene),  
 transformed by electroporation into DH10B cells (in  
 vitro) for propagation"

## FEATURES

ORIGIN

```

Query Match 65.3%; Score 480.8; DB 8; Length 610;  

Best Local Similarity 93.6%; Pred. No. 1.3e-139;  

Matches 510; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
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185 GTGATCTTCATCAAG 244  
 1 GTGATCTTCATTCATGAGATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60  
 245 ATAAAG 304  
 61 ATAAAG 120  
 305 CACCAAG 364  
 121 CACCAAG 180  
 365 ATTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421  
 181 ATTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 422 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481  
 241 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 482 CCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 541  
 301 CCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
 542 GTGATCCCAAG 601  
 361 GTGATCCCAAG 420  
 602 CAGAGTCCCAAG 661  
 421 CAGAGTCCCAAG 480

QY 662 ATCCCACTATCTTCGCAAGACCCCTCTCTATATAGGAAGTTCAATTCATTGGAGA 721  
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 QY 481 ATCCCACTATCTTCGCAAGACCCCTCTCTATATAGGAAGTTCAATTCATTGGAGA 540  
 Db |||||  
 QY 722 GACCA 726  
 Db |||||  
 QY 541 GACCA 545

## RESULT 11

CX308688 733 bp mRNA linear EST 06-MAY-2005  
 LOCUS C21002G02Rv AbeLeasub1 Citrus clementina cDNA clone C21002G02, mRNA  
 sequence.

ACCESSION CX308688  
 VERSION CX308688.1 GI:63077542

KEYWORDS EST

SOURCE Citrus clementina

ORGANISM Citrus clementina

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Sapindales; Rutaceae; Citrus.

## AUTHORS

1 (bases 1 to 733)  
 Forment J., Gades, J., Huerta, L., Abizanda, L., Agusti, J., Alamar, S.,  
 Alos, E., Andres, F., Arribas, R., Beltran, J.P., Berbel, A.,  
 Blazquez, M.A., Brumos, J., Canas, L.A., Cercos, M.,  
 Colmenero-Flores, J.M., Conesa, A., Establies, B., Gandia, M.,  
 Gonzalez-Candel, J.L., Glamo, J., Gilbert, A., Gomez, G.,  
 Gonzalez-Fernandez, J., Gual, A., Herrero, J., Lafuente, M.T.,  
 Madueno, F., Marcos, J.F., Martinez, M.C., Matute, J., Navarro, L.,  
 Martinez-Godoy, M.A., Miralles, S., Moreno, P., Navarro, L., Pallas, V.,  
 Perez-Amador, M.A., Perez-Valle, J., Pons, C., Rodrigo, I.,  
 Rodriguez, P.L., Royo, C., Serrano, R., Soler, G., Tadeo, F., Talon, M.,  
 Terol, J., Trenor, M., Vaeillo, L., Vicente, O., Vidal, Ch., Zacarias, L.,  
 and Conejero, V.

## TITLE

Development of a citrus genome-wide EST collection and cDNA

microarray as resources for genomic studies

Plant Mol. Biol. 57 (3), 375-391 (2005)

## JOURNAL

PUBLISHED Contact: Forment J

COMMENT Genomics Laboratory

Unit of Citrus Molecular Biology

Universitat de Valencia

Politecnica de Valencia - Consejo Superior de Investigaciones

Cientificas

Avenida de los Naranjos s/n, 46022 Valencia, Spain

Email: jforment@bmcp.upv.es

Location/Qualifiers

1..733

/organism="Citrus clementina"

/mol\_type="mRNA"

/cultivar="Clementine"

/db\_xref="taxon:85681"

/date="20050208"

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/dev\_stage="adult trees"

/lab\_host="Escherichia coli"

/clone\_lib="AbeLeasub1"

/notes="Organ: leaves; Vector: pCR2.1; Subtracted cDNA  
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## ORIGIN

Query Match 60.8%; Score 447.2; DB 8; Length 733;  
 Best Local Similarity 84.8%; Pred. No. 5.3e-129;  
 Matches 543; Conservative 0; Mismatches 28; Indels 69; Gaps 1;

QY 121 AGTCGACTTTTCACAAAGGTTATATCGGAAGCTCTCGAGTTCGATTCGATTCGCT 180

Db |||||

QY 94 ATTGAGCTTTTCACAAAGGTTATATCGGAAGCTCTCGAGTTCGATTCGATTCGCT 193

Db |||||

QY 181 ATCTGTCACTTTCACAAAGGTTATATCGGAAGGTTGACCTTCAAAATGCCATCAT 240

Db |||||

QY 154 ATCTGTCACTTTCACAAAGGTTATATCGGAAGGTTGACCTTCAAAATGCCATCAT 213

Db |||||

QY 241 TCGGATAAAGGAAGGCTATCGTTCAAGATSCCTCTGCGCAGATGTCGCCAAGATGGA 300  
 Db |||||  
 QY 214 TCGGATAAAGGAAGGCGCATCGTTGGAAGATGCTCTGCGCAGATGTCGCCAAGATGGA 273  
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 QY 334 GTGGATTGATGATGATGCGAGCAGCAGACACACTTGTCTTCTACTCCAAATATCAAA 393  
 Db |||||  
 QY 379 -----AGTGAGACTTTTCAACAAAGGTTAATATCGGA 411  
 Db |||||  
 QY 394 GATAGATCTCAGAGACCAAAAGGCGCAATGAGAGCTTTTCAACAAAGGTTAATATCGGA 453  
 Db |||||  
 QY 412 AACCTCTCGGATTCATTCGCCAGCTTATCTGTCTACTTCATCAAAAGGACAGTAGAAAG 471  
 Db |||||  
 QY 454 AACCTCTCGGATTCATTCGCCAGCTTATCTGTCTACTTCATCAAAAGGTTAATATCGGA 513  
 Db |||||  
 QY 472 GAAGTGGCAGCTACCAATGCCATCTCCGATTAAGGAAGGCTATCTTCAAGTCC 531  
 Db |||||  
 QY 514 GAAGTGGCTCTACCAATGCCATCTCCGATTAAGGAAGGCTATCTTCAAGTCC 573  
 Db |||||  
 QY 532 TCTGCCAGATGGTCCCAAGATGAGACCCACCCACGAGGAGATCTGTGGAAGAAAGAA 591  
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 QY 574 TCTGCCAGATGGTCCCAAGATGAGACCCACCCACGAGGAGATCTGTGGAAGAAAGAA 633  
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 QY 592 GAGCTTCACCAAGCTTCTTCAAGGAAGTGGATGATGATATCTTCAAGTCAAGG 651  
 Db |||||  
 QY 634 GAGTGGCAGCTTCCCTATCTCTGAGGAGGTTGATGATATCTTCAAGTCAAGG 693  
 Db |||||  
 QY 652 GAGTGGCAGCTTCCCTATCTCTGAGGAGGTTGATGATATCTTCAAGTCAAGG 691  
 Db |||||  
 QY 694 GATGAGGAGCTTCCCTATCTCTGAGGAGGTTGATGATATCTTCAAGTCAAGG 733  
 Db |||||

## RESULT 12

DN381521/c

LOCUS DN381521 738 bp mRNA linear EST 07-MAR-2005

DEFINITION LIB38534\_042\_E11\_T7\_1 LIB38534 Canis familiaris cDNA clone

ACCESSION LIB38534\_42\_E11 mRNA sequence.

VERSION DN381521

KEYWORDS EST

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Pissipedia; Canidae;  
 Canis.

REFERENCE 1 (bases 1 to 738)

Statens, N.R.

Direct Submission (Statens, N.R.)

Unpublished (2005)

JOURNAL

COMMENT

Contact: Nick Statens

Telephone: +45 8952 6892

Email: nicholas.statens@finzer.com

Location/Qualifiers

1..738

/organism="Canis familiaris"

/mol\_type="mRNA"

/db\_xref="taxon:9615"

/clone="LIB38534\_42\_E11"

/tissue\_type="unknown"

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/notes="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI"

## ORIGIN

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 Best Local Similarity 96.0%; Pred. No. 1e-115;  
 Matches 427; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

**Tue Jun 6 08:26:40 2006**

us-10-075-105c-1.rst

Page 10

[illegible][illegible]

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RESULT 13
DNB81910/c      DN881910      685 bp      mRNA      linear      EST 07-MAR-2005
LOCUS           L1B38534_041.COI_T7.1_L1B38534_Canis familiaris cDNA clone
DEFINITION      L1B38534_41.COI, mRNA sequence.
ACCESSION       DN81910
VERSION         DN81910.1   GI:60561310
KEYWORDS        EST
SOURCE          Canis familiaris (dog)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Laurasiatheria; Carnivora; Placentalia; Canidae
                 Canis.
REFERENCE       1 (bases 1 to 685)
AUTHORS         Staten N.R.
TITLE           Direct Substitution (Staten,N.R.)
JOURNAL         J Biol Chem
COMMENT         Contact: Nick Staten
                 Tel.: 616 247 6855
                 Email: nicholas.r.staten@pfizer.com.
FEATURES             Location/Qualifiers
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                     /clone=L1B38534_41.COI"
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ORIGIN

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RESULT	14
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DEFINITION	A0662115 DNA linear GSS 03-FEB-1995 mgxb0003728f CGEI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0003728f, genomic survey sequence.
ACCESION	A0662115
VERSION	A0662115.1 GI:#421034
SOURCE	GSS
ORGANISM	Magnaporthe grisea (anamorph: Pyricularia grisea)
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportaceae; Magnaporthe. 1 (basea 1 to 833) Yu,Y., Zhu,H., Boyd,C.A., Gaudetle,B., Gayle,A., Kingsbury,R., Phillips,K.J., Santowski,M., Wang,S.R. and Dean,R.A. A BAC end sequencing framework to sequence the Magnaporthe grisea genome unpublished (1998)
JOURNAL COMMENT	Contact : Dean RA Clemson University Genomic Institute Clemson University 100 Jordan Hall, Clemson University, Clemson, SC 29634  Tel.: 864 656 5797 Fax: 864 656 4293 Email : dean@clermson.edu Small : jreagan@cact.cactatnrgsc Class: BAC ends High quality sequence start: 58 High quality sequence stop: 454. Location/Qualifiers 1 .. 839
FEATURES	
SOURCE	

	Query Match	98.1%	Score 354	DB 9	Length 685
	Best Local Similarity	95.4%	Pred. No. 1.1e-99		
	Matches 376:	Conservative	0	Mismatches 15	Indels 3; Gaps 1
Dy	341	CACCACTCTTCAACAAGATGATGATGATTC---AGTAGACTTTTCAAAA	397		
Db	685	CACCACTCTTCAACAAGAATGATGATGATGCAGATTGAAGCTTTTCAAAA	626		

[illegible]

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/mol_type="Genomic DNA"  
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/date_issued="70-15"  
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/feature_type="vector_clone"  
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/notes="Vector: pBACRIC; Site 1: HindIII; Site 2: HindIII;  
Rice blast is one of the most devastating fungal diseases  
of rice world wide. It is a filamentous ascomycete with  
a haploid genome (n=7) of approximately 40 Mbp. Rice  
blast is an important model fungal pathogen for studying  
numerous aspects of the fungal-host interaction. In  
order to facilitate genome wide analysis, a BAC library  
containing 936 clones with an average insert size of 130  
kbp was constructed. This library represents greater
```

than 25X genome coverage. High density colony filters  
are available upon request."

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ORIGIN
Query Match 47.8%; Score 351.8; DB 11; Length 839;
Best Local Similarity 99.4%; Pred. No. 68-99; 2; Indels 0; Gaps 0;
Matches 353; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 379 AGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATATGCCAGCT 438
Db 163 ATTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATATGCCAGCT 222
QY 439 ATCTGTCACTTCACTCAAAAGGACAGTAGAAGAGAGGTGGCACTTCAAAATGCCATCAT 498
Db 223 ATCTGTCACTTCACTCAAAAGGACAGTAGAAGAGAGGTGGCACTTCAAAATGCCATCAT 282
QY 499 TCGGATTAAGGAAAGGCTATCTTCAAGTCTCTCTCGGACAGTGTGCCAAAGATGGA 558
Db 283 TCGGATTAAGGAAAGGCTATCTTCAAGTCTCTCTCGGACAGTGTGCCAAAGATGGA 342
QY 559 CCCCCACCCACGAGGAGCATGTGGAAAAAGAGAGCTTCCACACAGCTCTTCAAGCAA 618
Db 343 CCCCCACCCACGAGGAGCATGTGGAAAAAGAGAGCTTCCACACAGCTCTTCAAGCAA 402
QY 619 GTGGATTGATGATATCTCCACTGACGTAAAGGAGTAGGCAACATCCCACTATCTTCG 678
Db 403 GTGGATTGATGATATCTCCACTGACGTAAAGGAGTAGGCAACATCCCACTATCTTCG 462
QY 679 CAGACCTTCTCTTATATAAGGAGTTCATTTTGGAGAGGACACCTGGA 733
Db 463 CAGACCTTCTCTTATATAAGGAGTTCATTTTGGAGAGGACACCTGGA 517

RESULT 15
CW799882
LOCUS
DEFINITION
WiscsLox391F04 Arabidopsis thaliana T-DNA insertion flanking
sequences Arabidopsis thaliana genomic, genomic survey sequence.
CW799882
CW799882.1 GI:55997710
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Spermatophytes; Embryophyta; Tracheophyta;
Spermatophytes; Embryophyta; Tracheophyta;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 869)
Woody, S.T., Monson, S.S., Jester, P.J., Austin-Phillips, S.,
Amasino, R.M., Sussman, M.R. and Krysan, P.J.
A New Community Resource for Knocking-Out Small Genes and
Randomly-Duplicated Gene Families and for Mosaic Analysis in
Arabidopsis
Unpublished (2004)
Contact: Woody St
Biotechnology Center
University of Wisconsin-Madison
425 Henry Mall, Madison, WI 53706, USA
Tel.: (608) 262-4640
Email: swoody@facstaff.wisc.edu
Class: TAIL-PCR.
Location/Qualifiers
1..869
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/db_xref="taxon:3702"
/tissue_type="seeds produced by primary (Basta-resistant)
transformants"
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sequences"
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of an Arabidopsis T-DNA tagging program. TAIL-PCR was used
to generate sequencing templates that represent A.T.

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ORIGIN
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Best Local Similarity 99.7%; Pred. No. 1.3e-96;
Matches 345; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 439 ATCTGTCACTTCACTCAAAAGGACAGTAGAAGAGAGGTGGCACTTCAAAATGCCATCAT 498
Db 173 ATCTGTCACTTCACTCAAAAGGACAGTAGAAGAGAGGTGGCACTTCAAAATGCCATCAT 232
QY 499 TCGGATTAAGGAAAGGCTATCTTCAAGTCTCTCTCGGACAGTGTGCCAAAGATGGA 558
Db 233 TCGGATTAAGGAAAGGCTATCTTCAAGTCTCTCTCGGACAGTGTGCCAAAGATGGA 292
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Db 293 CCCCCACCCACGAGGAGCATGTGGAAAAAGAGAGCTTCCACACAGCTCTTCAAGCAA 352
QY 619 GTGGATTGATGATATCTCCACTGACGTAAAGGAGTAGGCAACATCCCACTATCTTCG 678
Db 353 GTGGATTGATGATATCTCCACTGACGTAAAGGAGTAGGCAACATCCCACTATCTTCG 412
QY 679 CAGACCTTCTCTTATATAAGGAGTTCATTTTGGAGAGGA 724
Db 413 CAGACCTTCTCTTATATAAGGAGTTCATTTTGGAGAGGA 458

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